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OM protein - protein search, using sw model

Run on: October 22, 2001, 16:03:50 ; Search time 13.88 Seconds
(without alignments)
1192.697 Million cell updates/sec

Title: us-09-116-676-10

Perfect score: 4363

Sequence: 1 MICQKFCVLLHWEFIYVIT.....WLRISVVKKYIHGKFTIL 804

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	4337	99.4	1165	2	US-08-599-455B-4
2	4325	99.1	898	2	US-08-693-697-36
3	4325	99.1	908	2	US-08-693-697-33
4	4325	99.1	960	1	US-08-355-888A-8
5	4325	99.1	960	2	US-08-693-697-8
6	4325	99.1	960	2	US-08-640-389A-3
7	4325	99.1	960	3	US-08-693-696-8
8	4320	99.0	960	2	US-08-588-190-3
9	4315	98.9	908	2	US-08-588-526-3
10	4309	98.8	1165	2	US-08-640-389A-11
11	4297	98.5	896	2	US-08-640-389A-10
12	4297	98.5	906	2	US-08-640-389A-9
13	4297	98.5	958	2	US-08-640-389A-8
14	4261	77.0	896	2	US-08-640-389A-12
15	3345	76.7	894	2	US-08-599-455B-2
16	3345	76.7	1162	2	US-08-599-455B-43
17	3057	70.1	569	1	US-08-306-231-3
18	277.5	6.4	488	2	US-08-599-455B-5
19	277.5	6.4	658	2	US-08-825-558-4
20	277.5	6.4	708	1	US-07-797-556-2
21	277.5	6.4	708	1	US-08-308-881-2
22	277.5	6.4	708	2	US-09-058-263-2
23	277.5	6.4	708	2	US-09-059-099-2
24	277.5	6.4	708	3	US-09-058-264-2
25	277.5	6.4	708	5	PCT-US95-06530-2
26	277.5	6.4	918	2	US-08-825-558-6
27	246.5	5.6	837	1	US-07-923-976-2

28	242.5	5.6	771	1	US-07-923-976-6
29	242.5	5.6	783	6	5422248-2
30	242.5	5.6	836	1	US-07-923-976-4
31	242.5	5.6	863	1	US-07-923-976-8
32	221.5	5.1	1001	1	US-07-797-556-6
33	221.5	5.1	1001	1	US-07-943-843-2
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41	212.5	4.9	979	5	PCT-US95-06530-6
42	211	4.8	602	2	US-08-419-652-6
43	208	4.8	719	1	US-07-943-843-4
44	208	4.8	719	1	US-08-347-003-4
45	200.5	4.6	862	2	US-08-685-118-2

ALIGNMENTS

RESULT 1
US-08-599-455B-4
; Sequence 4, Application US/08599455B
; Patent No. 5972621
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
; TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,455B
FILING DATE: 22-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/017001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
TOPOLOGY: unknown

MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-599-455B-4

Query Match 99.4%; Score 4337; DB 2; Length 1165;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 MICQKFCVLLHWEFIYVITAFNLSYPTTPWRFKLSQMPNPNSTYDYFLLPAGLSKNTSNS 60
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Db 61 NGHYETAPEPKFNSGTHFSNLSKTTFFHCCFRSEQDRNCSLCADNIEGRTFVSTVNSLVF 120
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Db 121 QOIDANNIOCWLGDKLKFICYVESLFKNLFNRYNYKVHLLYVLPVLEDSPLVPQKGS 180
QY 181 FQVHCNCSVHECECLVPVPTAKLNDTLLMCLKITSGVIFQSPPLMSVQPINMKVPDPP 240
Db 181 FQVHCNCSVHECECLVPVPTAKLNDTLLMCLKITSGVIFQSPPLMSVQPINMKVPDPP 240
QY 241 LGLHMETDDGNLKSWSPPPLVPPFLOQYQVYKYSNSTTVIREADKIVSATSLLVDSILP 300
Db 241 LGLHMETDDGNLKSWSPPPLVPPFLOQYQVYKYSNSTTVIREADKIVSATSLLVDSILP 300
QY 301 GSSYEVOVQKRLDGPINSDNSTPRVFTTQDVIYFPKILTSVGSNVSFHCYKKNKI 360
Db 301 GSSYEVOVQKRLDGPINSDNSTPRVFTTQDVIYFPKILTSVGSNVSFHCYKKNKI 360
QY 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFNENETPKRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFNENETPKRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNIINISCTDGYLTRKTCRNSTSTIQSLAESTLQRLYHRSSLYCSDIPSIIH 480
Db 421 RYAEIYVIDVNIINISCTDGYLTRKTCRNSTSTIQSLAESTLQRLYHRSSLYCSDIPSIIH 480
QY 481 PISEPKCYLQSDGFEYECIFQPIFLLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKCYLQSDGFEYECIFQPIFLLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINTGLKISWEKVPFPENNIFQIRYGLSGKEVQWKMYEYVDKSKSVSLPV 600
Db 541 SSVKAEITINTGLKISWEKVPFPENNIFQIRYGLSGKEVQWKMYEYVDKSKSVSLPV 600
QY 601 PDLCAVAVQVRCRDLGLGYWNSNPNAYTVVMDIKVPMRGPEFWRIIDGDTMKKEKNV 660
Db 601 PDLCAVAVQVRCRDLGLGYWNSNPNAYTVVMDIKVPMRGPEFWRIIDGDTMKKEKNV 660
QY 661 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTWSVDGNHTKFTFLWTEQAHVTYVLAINSI 720
Db 661 TLLMKPLMKNDSLCSVQRYVINHHTSCNGTWSVDGNHTKFTFLWTEQAHVTYVLAINSI 720
QY 721 GASVANFNLTSPWPKSNVYVQSLAYSAYPLNSCVIVSWILSPSDYKLMYFIENKLNLED 780
Db 721 GASVANFNLTSPWPKSNVYVQSLAYSAYPLNSCVIVSWILSPSDYKLMYFIENKLNLED 780
QY 781 GEIKWLRISSSVKVKYIHGKF 801
Db 781 GEIKWLRISSSVKVKYIHDHF 801

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RESULT 2

US-08-693-697-36
Sequence 36, Application US/08693697
Patent No. 5869610
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph

```

APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,697
FILING DATE: 05-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0037-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 898 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-693-697-36

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Query Match 99.1%; Score 4325; DB 2; Length 898;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Db 3 MICQKFCVLLHWEFIYVITAFNLSYPTTPWRFKLSQMPNPNSTYDYFLLPAGLSKNTSNS 62
QY 61 NGHYETAPEPKFNSGTHFSNLSKTTFFHCCFRSEQDRNCSLCADNIEGRTFVSTVNSLVF 120
Db 63 NGHYETAPEPKFNSGTHFSNLSKTTFFHCCFRSEQDRNCSLCADNIEGRTFVSTVNSLVF 122
QY 121 QOIDANNIOCWLGDKLKFICYVESLFKNLFNRYNYKVHLLYVLPVLEDSPLVPQKGS 180
Db 123 QOIDANNIOCWLGDKLKFICYVESLFKNLFNRYNYKVHLLYVLPVLEDSPLVPQKGS 182
QY 181 FQVHCNCSVHECECLVPVPTAKLNDTLLMCLKITSGVIFQSPPLMSVQPINMKVPDPP 240
Db 183 FQVHCNCSVHECECLVPVPTAKLNDTLLMCLKITSGVIFQSPPLMSVQPINMKVPDPP 242
QY 241 LGLHMETDDGNLKSWSPPPLVPPFLOQYQVYKYSNSTTVIREADKIVSATSLLVDSILP 300
Db 243 LGLHMETDDGNLKSWSPPPLVPPFLOQYQVYKYSNSTTVIREADKIVSATSLLVDSILP 302
QY 301 GSSYEVOVQKRLDGPINSDNSTPRVFTTQDVIYFPKILTSVGSNVSFHCYKKNKI 360
Db 303 GSSYEVOVQKRLDGPINSDNSTPRVFTTQDVIYFPKILTSVGSNVSFHCYKKNKI 362
QY 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFNENETPKRGKFTYDAVYCCNEHECHH 420
Db 363 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFNENETPKRGKFTYDAVYCCNEHECHH 422
QY 421 RYAEIYVIDVNIINISCTDGYLTRKTCRNSTSTIQSLAESTLQRLYHRSSLYCSDIPSIIH 480

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Db 423 RYAEIYVIDVNIINISCTDGLTKMTCTRWSTIQSLAESTLQLRHRSLSYCDIPSIH 482
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 483 PISEPKDCYLQSDGFYECIFQPIFLLSGYTWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 542
QY 541 SSVKAEITINIGLLKISWEKPVPPENNLOFQIRYGLSGKEVQWKMYEYDAKSKVSLPV 600
Db 543 SSVKAEITINIGLLKISWEKPVPPENNLOFQIRYGLSGKEVQWKMYEYDAKSKVSLPV 602
QY 601 PDLCAVAVQVRCKRLDGLGYWNSNPATVYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 603 PDLCAVAVQVRCKRLDGLGYWNSNPATVYVMDIKVPMRGPEFWRIINGDTMKKEKNV 662
QY 661 TLLWPKLKMNDLSLCSVQRYVINHHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 663 TLLWPKLKMNDLSLCSVQRYVINHHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI 722
QY 721 GASVANFNLTFSWPMKVNIVQSLAYSAYPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 780
Db 723 GASVANFNLTFSWPMKVNIVQSLAYSAYPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 782
QY 781 GEIKWLRISSSVKYYIHGKF 801
Db 783 GEIKWLRISSSVKYYIHDF 803

RESULT 3

US-08-693-697-33
; Sequence 33, Application US/08693697
; Patent No. 5869610
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,697
; FILING DATE: 05-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Polissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0037-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 908 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-693-697-33

Query Match 99.1%; Score 4325; DB 2; Length 908;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSPITPWRFKLSCMPNPNSTYDFLLPAGLSKNTS 60
Db 3 MICQKFCVLLHWEFIYVITAFNLSPITPWRFKLSCMPNPNSTYDFLLPAGLSKNTS 62
QY 61 NGHYETAPEPKFNSSSTHPSNLSTKTFHCCFRSEQRNCSLACADNTEGKTFVTVNSLVP 120
Db 63 NGHYETAPEPKFNSSSTHPSNLSTKTFHCCFRSEQRNCSLACADNTEGKTFVTVNSLVP 122
QY 121 QQIDANNITQCLWLGDLKLFICVYESLFKNLFNRYNKKVHLLVYLPVLEDSPLVPQKGS 180
Db 123 QQIDANNITQCLWLGDLKLFICVYESLFKNLFNRYNKKVHLLVYLPVLEDSPLVPQKGS 182
QY 181 FQVHCNCSVHECCCLVPPVPTAKLNDTLMLCLKITSGGVIFOSPLMSVQPINNVKPDPP 240
Db 183 FQVHCNCSVHECCCLVPPVPTAKLNDTLMLCLKITSGGVIFOSPLMSVQPINNVKPDPP 242
QY 241 LGLHMEITDDGNLKISSWSPPLVPFPLOVQVYSENSTTVIREADKIVSATSLVDSILP 300
Db 243 LGLHMEITDDGNLKISSWSPPLVPFPLOVQVYSENSTTVIREADKIVSATSLVDSILP 302
QY 301 GSSYEYQVRGKRLDGPGLMSDWSSTPRVFTTQDVIYPPPKILTSVGNVSPFHCYKKNKI 360
Db 303 GSSYEYQVRGKRLDGPGLMSDWSSTPRVFTTQDVIYPPPKILTSVGNVSPFHCYKKNKI 362
QY 361 VPSKEIVWMNLAEKIPQSOYDVVSDHVSKVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
Db 363 VPSKEIVWMNLAEKIPQSOYDVVSDHVSKVTFEFLNETKPRGKFTYDAVYCCNEHECHH 422
QY 421 RYAEIYVIDVNIINISCTDGLTKMTCTRWSTIQSLAESTLQLRHRSLSYCDIPSIH 480
Db 423 RYAEIYVIDVNIINISCTDGLTKMTCTRWSTIQSLAESTLQLRHRSLSYCDIPSIH 482
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 483 PISEPKDCYLQSDGFYECIFQPIFLLSGYTWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 542
QY 541 SSVKAEITINIGLLKISWEKPVPPENNLOFQIRYGLSGKEVQWKMYEYDAKSKVSLPV 600
Db 543 SSVKAEITINIGLLKISWEKPVPPENNLOFQIRYGLSGKEVQWKMYEYDAKSKVSLPV 602
QY 601 PDLCAVAVQVRCKRLDGLGYWNSNPATVYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 603 PDLCAVAVQVRCKRLDGLGYWNSNPATVYVMDIKVPMRGPEFWRIINGDTMKKEKNV 662
QY 661 TLLWPKLKMNDLSLCSVQRYVINHHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 663 TLLWPKLKMNDLSLCSVQRYVINHHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI 722
QY 721 GASVANFNLTFSWPMKVNIVQSLAYSAYPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 780
Db 723 GASVANFNLTFSWPMKVNIVQSLAYSAYPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 782
QY 781 GEIKWLRISSSVKYYIHGKF 801
Db 783 GEIKWLRISSSVKYYIHDF 803

RESULT 4

US-08-355-888A-8
; Sequence 8, Application US/08355888A
; Patent No. 5763211
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN

; TITLE OF INVENTION: RECEPTOR
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/355,888A
 ; FILING DATE: 14-DEC-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Poissant, Brian M.
 ; REGISTRATION NUMBER: 28,462
 ; REFERENCE/DOCKET NUMBER: 7225-078
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 960 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-355-888A-8

Query Match 99.1%; Score 4325; DB 1; Length 960;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY	1	MICQKFCVLLHWEIYVITAFNLSPYTPWRFKLSCLMPPNSTYDFLLPAGLSKNTSNS	60
DB	3	MICQKFCVLLHWEIYVITAFNLSPYTPWRFKLSCLMPPNSTYDFLLPAGLSKNTSNS	62
QY	61	NGHYETAVEPFNSGTHFNSLKTFFCCPSEODRNCSCADNIEGKTFVSTVNSLVF	120
DB	63	NGHYETAVEPFNSGTHFNSLKTFFCCPSEODRNCSCADNIEGKTFVSTVNSLVF	122
QY	121	QOIDANNIOCLKGLDLKLFICYVESLEKFLFRNYKVVHLLYVLPVLEDSPLVPQKS	180
DB	123	QOIDANNIOCLKGLDLKLFICYVESLEKFLFRNYKVVHLLYVLPVLEDSPLVPQKS	182
QY	181	FQVHCNCSVHECCCLVPVPTAKLNDLMLCLKITSGVIFQSPMSVQPINNVKPDPP	240
DB	183	FQVHCNCSVHECCCLVPVPTAKLNDLMLCLKITSGVIFQSPMSVQPINNVKPDPP	242
QY	241	LGLHMETDDGNLKSWSPLPFPFQYQVYKYSNSTTIVREADKIVSATSLVDSILP	300
DB	243	LGLHMETDDGNLKSWSPLPFPFQYQVYKYSNSTTIVREADKIVSATSLVDSILP	302
QY	301	GSSYEYQVGRKRLDGPGLWSDMSTPRVFTTODVIFPFPKILTSVGSNVSFHCIIYKKNKI	360
DB	303	GSSYEYQVGRKRLDGPGLWSDMSTPRVFTTODVIFPFPKILTSVGSNVSFHCIIYKKNKI	362
QY	361	VPSKEIVVMNNAEKIPQSQDYVSDHVSQVTFNKLNETKPRGFTYDAVYCCNEHCCH	420
DB	363	VPSKEIVVMNNAEKIPQSQDYVSDHVSQVTFNKLNETKPRGFTYDAVYCCNEHCCH	422
QY	421	RYAELXYVDVNNISCTDGYLTWMTCRWSTSTTQSLAESTLQRYHRSSLYCSDIPSII	480
DB	423	RYAELXYVDVNNISCTDGYLTWMTCRWSTSTTQSLAESTLQRYHRSSLYCSDIPSII	482
QY	481	PISPKDCYVLSQDGFYECIFQPIFLLSGYTWMIRINHSLGSLDSPPTCVLPDSVVKPLPP	540

DB	483	PISPKDCYVLSQDGFYECIFQPIFLLSGYTWMIRINHSLGSLDSPPTCVLPDSVVKPLPP	542
QY	541	SSVKABITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQMKMYEYVYDAKSKSVSLPV	600
DB	543	SSVKABITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQMKMYEYVYDAKSKSVSLPV	602
QY	601	PDLCAVYAVQVRCKRLDGLGYWSNNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKKNV	660
DB	603	PDLCAVYAVQVRCKRLDGLGYWSNNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKKNV	662
QY	661	TLWKPLMKNDSLCSVQRYVINHHTSCNGTWSDEYGNHTKFTFLTEQAHTVTVLAINSI	720
DB	663	TLWKPLMKNDSLCSVQRYVINHHTSCNGTWSDEYGNHTKFTFLTEQAHTVTVLAINSI	722
QY	721	GASVANFNLTFSWPMKSNVIVOSLSAYPLNNSCVIVSWILSPSDYKLMYFIIEWNLNED	780
DB	723	GASVANFNLTFSWPMKSNVIVOSLSAYPLNNSCVIVSWILSPSDYKLMYFIIEWNLNED	782
QY	781	GEIKWLRISSSVKKYIHKGF 801	
DB	783	GEIKWLRISSSVKKYIHKGF 803	

RESULT 5
 US-08-693-697-8
 ; Sequence 8, Application US/08693697
 ; Patent No. 5869610
 ; GENERAL INFORMATION:
 ; APPLICANT: Snodgrass, H. R.
 ; APPLICANT: Cioffi, Joseph
 ; APPLICANT: Zupancic, Thomas J.
 ; APPLICANT: Shafer, Alan W.
 ; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
 ; TITLE OF INVENTION: RECEPTOR
 ; NUMBER OF SEQUENCES: 38
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/693,697
 ; FILING DATE: 05-AUG-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Poissant, Brian M.
 ; REGISTRATION NUMBER: 28,462
 ; REFERENCE/DOCKET NUMBER: 8907-0037-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-493-4935
 ; TELEFAX: 650-493-5556
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 960 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-693-697-8

Query Match 99.1%; Score 4325; DB 2; Length 960;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEIYVITAFNLSPYTPWRFKLSCLMPPNSTYDFLLPAGLSKNTSNS 60

Db 3 MICQFCVLLHWEFIIYITAFNLSYPIITPWFREKLSMPNPNSTYDFLLPAGLSKNTS 62
QY 61 NGHETAVEPKFNSGTHFNSLSTTFFHCCFRSDQNRNCSLCADNIEGKTFVSTVNSLVF 120
Db 63 NGHETAVEPKFNSGTHFNSLSTTFFHCCFRSDQNRNCSLCADNIEGKTFVSTVNSLVF 122
QY 121 QOIDANNIOCLWGLDKLFCYVESLFKLFNRYNKVHLLYVLPVLEDSPLVPKGS 180
Db 123 QOIDANNIOCLWGLDKLFCYVESLFKLFNRYNKVHLLYVLPVLEDSPLVPKGS 182
QY 181 FQVHCNCSVHECECLVPVPTAKLNDTLMLCKITSGGVIFOSPLMSVQPINNVKPDPP 240
Db 183 FQVHCNCSVHECECLVPVPTAKLNDTLMLCKITSGGVIFOSPLMSVQPINNVKPDPP 242
QY 241 LGLHMETDGNLKSISWSSPPLVPFPLOQYQVYSENSTTVIREADKIVSATSLLVDSILP 300
Db 243 LGLHMETDGNLKSISWSSPPLVPFPLOQYQVYSENSTTVIREADKIVSATSLLVDSILP 302
QY 301 GSSYEVOVRKRLDGGPGIWSDMSTPRVFTTQDVIYFPFKILTSGVNSVPHCIYKKNKI 360
Db 303 GSSYEVOVRKRLDGGPGIWSDMSTPRVFTTQDVIYFPFKILTSGVNSVPHCIYKKNKI 362
QY 361 VPSKEIWMNLAEKIPQSOYDVVSDHVSQVTFNENETKPRGKFTYDGVYCCNEHECHH 420
Db 363 VPSKEIWMNLAEKIPQSOYDVVSDHVSQVTFNENETKPRGKFTYDGVYCCNEHECHH 422
QY 421 RYAEIYVIDVNIINISCTDGYLTGKMTCRWSTSTIQSLAESTLQLRVHRSSLYCSDIPSIIH 480
Db 423 RYAEIYVIDVNIINISCTDGYLTGKMTCRWSTSTIQSLAESTLQLRVHRSSLYCSDIPSIIH 482
QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
Db 483 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 542
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKYEVYDAKSKSVSLPV 600
Db 543 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKYEVYDAKSKSVSLPV 602
QY 601 PDLCAVAVQVRKRLDGLGYSWNSNPAVTVVMDIKVPMRGPEFWIRIINGDTMKKEKNV 660
Db 603 PDLCAVAVQVRKRLDGLGYSWNSNPAVTVVMDIKVPMRGPEFWIRIINGDTMKKEKNV 662
QY 661 TLLWKLPMKNDLSQVQRYVINHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 663 TLLWKLPMKNDLSQVQRYVINHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI 722
QY 721 GASVANFNLTFSWPMKVNIVQSLSATPLNSSCVIYVSWILSPSDYKLMYFIIEMKNLNE 780
Db 723 GASVANFNLTFSWPMKVNIVQSLSATPLNSSCVIYVSWILSPSDYKLMYFIIEMKNLNE 782
QY 781 GEIKWLRISSSVKYYIHGKF 801
Db 783 GEIKWLRISSSVKYYIHDHF 803

RESULT 6

US-08-640-389A-3
; Sequence 3, Application US/08640389A
; Patent No. 5912123
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: DETECTION OF THE LEPTIN
; TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR
; TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY
; NUMBER OF SEQUENCE: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York

STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,389A
FILING DATE: 29-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-640-389A-3

Query Match 99.1%; Score 4325; DB 2; Length 960;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MICQFCVLLHWEFIIYITAFNLSYPIITPWFREKLSMPNPNSTYDFLLPAGLSKNTS 60
Db 3 MICQFCVLLHWEFIIYITAFNLSYPIITPWFREKLSMPNPNSTYDFLLPAGLSKNTS 62
QY 61 NGHETAVEPKFNSGTHFNSLSTTFFHCCFRSDQNRNCSLCADNIEGKTFVSTVNSLVF 120
Db 63 NGHETAVEPKFNSGTHFNSLSTTFFHCCFRSDQNRNCSLCADNIEGKTFVSTVNSLVF 122
QY 121 QOIDANNIOCLWGLDKLFCYVESLFKLFNRYNKVHLLYVLPVLEDSPLVPKGS 180
Db 123 QOIDANNIOCLWGLDKLFCYVESLFKLFNRYNKVHLLYVLPVLEDSPLVPKGS 182
QY 181 FQVHCNCSVHECECLVPVPTAKLNDTLMLCKITSGGVIFOSPLMSVQPINNVKPDPP 240
Db 183 FQVHCNCSVHECECLVPVPTAKLNDTLMLCKITSGGVIFOSPLMSVQPINNVKPDPP 242
QY 241 LGLHMETDGNLKSISWSSPPLVPFPLOQYQVYSENSTTVIREADKIVSATSLLVDSILP 300
Db 243 LGLHMETDGNLKSISWSSPPLVPFPLOQYQVYSENSTTVIREADKIVSATSLLVDSILP 302
QY 301 GSSYEVOVRKRLDGGPGIWSDMSTPRVFTTQDVIYFPFKILTSGVNSVPHCIYKKNKI 360
Db 303 GSSYEVOVRKRLDGGPGIWSDMSTPRVFTTQDVIYFPFKILTSGVNSVPHCIYKKNKI 362
QY 361 VPSKEIWMNLAEKIPQSOYDVVSDHVSQVTFNENETKPRGKFTYDGVYCCNEHECHH 420
Db 363 VPSKEIWMNLAEKIPQSOYDVVSDHVSQVTFNENETKPRGKFTYDGVYCCNEHECHH 422
QY 421 RYAEIYVIDVNIINISCTDGYLTGKMTCRWSTSTIQSLAESTLQLRVHRSSLYCSDIPSIIH 480
Db 423 RYAEIYVIDVNIINISCTDGYLTGKMTCRWSTSTIQSLAESTLQLRVHRSSLYCSDIPSIIH 482
QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
Db 483 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 542
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKYEVYDAKSKSVSLPV 600
Db 543 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKYEVYDAKSKSVSLPV 602

QY 601 PDLCAVAVQVRCRDLGLGYNSNSNPAYTVVMDIKVPMRGPEFWRIINGOTMKKEKNV 660
DB 603 PDLCAVAVQVRCRDLGLGYNSNSNPAYTVVMDIKVPMRGPEFWRIINGOTMKKEKNV 662
QY 661 TLWAKPLMKNDLSQVQRYVINHTSCNCTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI 720
DB 663 TLWAKPLMKNDLSQVQRYVINHTSCNCTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI 722
QY 721 GASVANFNLTFSWPMKSNVIVOSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNEED 780
DB 723 GASVANFNLTFSWPMKSNVIVOSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNEED 782
QY 781 GEIKWLRISSSVKYYIHGKF 801
DB 783 GEIKWLRISSSVKYYIHDF 803

RESULT 7

US-08-693-696-8
; Sequence 8, Application US/08693696
; Patent No. 6005080
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cloffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: HU-B1.219, A NOVEL HUMAN HEMATOPOIETIN
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693.696
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/355,888
; FILING DATE: 14-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 7225-078
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 960 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-693-696-8

Query Match 99.18; Score 4325; DB 3; Length 960;
Best Local Similarity 99.48; Pred. No. 0;
Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 MICQKFCVLLHWEFIYVITAFNLSYPTTPWRFLKSCMPNSTDYDILLPAGLSKNTSNS 60
DB 3 MICQKFCVLLHWEFIYVITAFNLSYPTTPWRFLKSCMPNSTDYDILLPAGLSKNTSNS 62

QY 61 NGHETAVPEPKFNSSCTHFSNLSKTTFHCCFRSEODRNSCLCADNTEGKTFYSTVNSLVF 120
DB 63 NGHETAVPEPKFNSSCTHFSNLSKATFHCCFRSEODRNSCLCADNTEGRTFYSTVNSLVF 122
QY 121 QOIDANWNTQCNLKGDKLFCYVESLSFKNLFRNFKVHLLYVLPVLEDSPLVPQKGS 180
DB 123 QOIDANWNTQCNLKGDKLFCYVESLSFKNLFRNFKVHLLYVLPVLEDSPLVPQKGS 182
QY 181 FQMVHCNSVHECCCLVPPTAKLNDTLMLCLKITSGVIFQSPMLSVQPINNVKPPDP 240
DB 183 FQMVHCNSVHECCCLVPPTAKLNDTLMLCLKITSGVIFQSPMLSVQPINNVKPPDP 242
QY 241 LGLHMEITDGNLKIWSWSPPLVPFPLOYQVYKSENSTTVIREADKIYSATSLLVDSILP 300
DB 243 LGLHMEITDGNLKIWSWSPPLVPFPLOYQVYKSENSTTVIREADKIYSATSLLVDSILP 302
QY 301 GSSYEVQVRGKRLDGPGLWSDWSTPRVFTQDVIYFPFKILTSVGSNVSFHCYKKNKI 360
DB 303 GSSYEVQVRGKRLDGPGLWSDWSTPRVFTQDVIYFPFKILTSVGSNVSFHCYKKNKI 362
QY 361 VPSKEIVMMNLAEKIPQSDVDVSDHVSQVTFNLTNETKPRGKFTYDAVYCCNHECHH 420
DB 363 VPSKEIVMMNLAEKIPQSDVDVSDHVSQVTFNLTNETKPRGKFTYDAVYCCNHECHH 422
QY 421 RYAEIYVIDVNIINISCTDGYLTMTCTWSTSTIQSLAESTLQRLYHRSSLYCSDIPSTH 480
DB 423 RYAEIYVIDVNIINISCTDGYLTMTCTWSTSTIQSLAESTLQRLYHRSSLYCSDIPSTH 482
QY 481 PISEPKDCYLQSDGEYECIFQPIFLLSGYTMWIRNHSGLSDSPPTCVLPDSVVKPLPP 540
DB 483 PISEPKDCYLQSDGEYECIFQPIFLLSGYTMWIRNHSGLSDSPPTCVLPDSVVKPLPP 542
QY 541 SSVKAEITINIGLLKISWEKVPENNLOFOIRYGLSKEVQWKMYEYDAKSKSVSLPV 600
DB 543 SSVKAEITINIGLLKISWEKVPENNLOFOIRYGLSKEVQWKMYEYDAKSKSVSLPV 602
QY 601 PDLCAVAVQVRCRDLGLGYNSNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
DB 603 PDLCAVAVQVRCRDLGLGYNSNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 662
QY 661 TLWAKPLMKNDLSQVQRYVINHTSCNCTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI 720
DB 663 TLWAKPLMKNDLSQVQRYVINHTSCNCTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI 722
QY 721 GASVANFNLTFSWPMKSNVIVOSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNEED 780
DB 723 GASVANFNLTFSWPMKSNVIVOSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNEED 782
QY 781 GEIKWLRISSSVKYYIHGKF 801
DB 783 GEIKWLRISSSVKYYIHDF 803

RESULT 8

US-08-588-190-3
; Sequence 3, Application US/08588190
; Patent No. 5856098
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. Ralph
; APPLICANT: Cloffi, Joseph
; APPLICANT: Zupancic, Thomas Joel
; APPLICANT: Shafer, Alan Wayne
; TITLE OF INVENTION: DETECTION OF A LEPTIN RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of The Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,190
FILING DATE: 18-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 008907-0029-999
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-588-190-3

Query Match 99.0%; Score 4320; DB 2; Length 960;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 795; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFYIVTAENLSYPTTPWRFKLSMPPNPNSTYDFLLPAGLSKNTS 60
DB 3 MICQKFCVLLHWEFYIVTAENLSYPTTPWRFKLSMPPNPNSTYDFLLPAGLSKNTS 62
QY 61 NGHYETAVEPKNSGTHFSNLSKTHCCFSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
DB 63 NGHYETAVEPKNSGTHFSNLSKTHCCFSEQDRNCSLCADNIEGKTFVSTVNSLVF 122
QY 121 QQIDANNITQCKLKGDLKFCYVESLFRNRYKVLHLYVLEVEDSPLVPQKGS 180
DB 123 QQIDANNITQCKLKGDLKFCYVESLFRNRYKVLHLYVLEVEDSPLVPQKGS 182
QY 181 FQVHCNCSVHECCCECLVPVPTAKLNDTLMLCKITSGVIFOSPLMSVQPINMVKPDP 240
DB 183 FQVHCNCSVHECCCECLVPVPTAKLNDTLMLCKITSGVIFOSPLMSVQPINMVKPDP 242
QY 241 LGLHMEITDGNLKITSSWSPPLVPVPPLOYQVYSENSTTVIREADKIVSATSLVDSILP 300
DB 243 LGLHMEITDGNLKITSSWSPPLVPVPPLOYQVYSENSTTVIREADKIVSATSLVDSILP 302
QY 301 GSSYEVQVGRKLDGPGIWSMDSTPRVFTTQDVYVFPKILTSGVSNVSHFCIYKKNKI 360
DB 303 GSSYEVQVGRKLDGPGIWSMDSTPRVFTTQDVYVFPKILTSGVSNVSHFCIYKKNKI 362
QY 361 VPSKEIVWNNLAEKIPQSQYQVSDVSHSVKVTFFENETKPRGKFTYDVCNHECHH 420
DB 363 VPSKEIVWNNLAEKIPQSQYQVSDVSHSVKVTFFENETKPRGKFTYDVCNHECHH 422
QY 421 RYAEIVYDVNINISCTDGYLTCTCRWSTSTIQSLAESTLQRLYHRSLSYCSIDPSIH 480
DB 423 RYAEIVYDVNINISCTDGYLTCTCRWSTSTIQSLAESTLQRLYHRSLSYCSIDPSIH 482
QY 481 PISEPKDCYQSDGVECFIQIFILLSGYTMWIRNHSLSGSDSPPTCVLPDSVVKPLPP 540
DB 483 PISEPKDCYQSDGVECFIQIFILLSGYTMWIRNHSLSGSDSPPTCVLPDSVVKPLPP 542
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGREVQKMYEYVDAKSKSVSLPV 600
DB 543 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGREVQKMYEYVDAKSKSVSLPV 602

QY 601 PDLCAVYAVQVRCKRLDGLGYNSNPNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
DB 603 PDLCAVYAVQVRCKRLDGLGYNSNPNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 662
QY 661 TLLWKPLMKNDLSLCSVQRYVINHTSCNCTWSEDVGNHKTFTFLMTEQAHVTVLAINSI 720
DB 663 TLLWKPLMKNDLSLCSVQRYVINHTSCNCTWSEDVGNHKTFTFLMTEQAHVTVLAINSI 722
QY 721 GASVANENLTFSWPMKVNIVQSLAYSPLNSCVIVSWILSPDYKLMYFIIENKLNED 780
DB 723 GASVANENLTFSWPMKVNIVQSLAYSPLNSCVIVSWILSPDYKLMYFIIENKLNED 782
QY 781 GEIKWLRISSVKKYIHGKF 801
DB 783 GEIKWLRISSVKKYIHDHF 803

RESULT 9
US-08-588-526-3
Sequence 3, Application US/08588526
Patent No. 5882860
GENERAL INFORMATION:
APPLICANT: Snodgrass, H.
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas
APPLICANT: Shafer, Alan
TITLE OF INVENTION: DETECTION OF A LEPTIN RECEPTOR
TITLE OF INVENTION: VARIANT
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds
CITY: 1155 Avenue of the Americas
STATE: New York
COUNTRY: US
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,526
FILING DATE: 18-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 908 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-588-526-3

Query Match 98.9%; Score 4315; DB 2; Length 908;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 794; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFYIVTAENLSYPTTPWRFKLSMPPNPNSTYDFLLPAGLSKNTS 60
DB 3 MICQKFCVLLHWEFYIVTAENLSYPTTPWRFKLSMPPNPNSTYDFLLPAGLSKNTS 62
QY 61 NGHYETAVEPKNSGTHFSNLSKTHCCFSEQDRNCSLCADNIEGKTFVSTVNSLVF 120

Db 63 NGHETAVEPEKFNSSGTHFNSLKHATFHCCFRSEQDRNCSLCADNIEGRTFVSTVNSLVF 122
QY 121 QOIDANNIOCLWKGDLKLFICVYESLFKRLFRNYKVHLLVYLPEVLEDSPLVPQKGS 180
Db 123 QOIDANNIOCLWKGDLKLFICVYESLFKRLFRNYKVHLLVYLPEVLEDSPLVPQKGS 182
QY 181 FQVHCNCSVHECCCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPMLSVQPINNVKPDPP 240
Db 183 FQVHCNCSVHECCCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPMLSVQPINNVKPDPP 242
QY 241 LGLHMETDDGNLKISWSSPPLVPFPLOQVQKYSNSTTVIRADKIVSATSLLVDSILP 300
Db 243 LGLHMETDDGNLKISWSSPPLVPFPLOQVQKYSNSTTVIRADKIVSATSLLVDSILP 302
QY 301 GSSYEVOVGRKRLDGGCGIWSGWTSPVFTTQDVVYPPPKILTSGVSNVSHFCIYKKNKI 360
Db 303 GSSYEVOVGRKRLDGGCGIWSGWTSPVFTTQDVVYPPPKILTSGVSNVSHFCIYKKNKI 362
QY 361 VPSKEIVWMNLAEKIPQSOYDVVSDHVSQVTFNLFNETKPRGKFTYDAVYCCNEHECHH 420
Db 363 VPSKEIVWMNLAEKIPQSOYDVVSDHVSQVTFNLFNETKPRGKFTYDAVYCCNEHECHH 422
QY 421 RYAEIYVIDVNIINISCTDGYLTMTKRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIH 480
Db 423 RYAEIYVIDVNIINISCTDGYLTMTKRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIH 482
QY 481 PISEPKDCYLOSDGFEYECIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
Db 483 PISEPKDCYLOSDGFEYECIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 542
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKNYEVYDAKSKSVSLPV 600
Db 543 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKNYEVYDAKSKSVSLPV 602
QY 601 POLCAVAVQVRCRDLGGLGYWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNY 660
Db 603 POLCAVAVQVRCRDLGGLGYWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNY 662
QY 661 TLLWPLMKNDLSCSVQRYVINHHSTSCNGTWSVDGNGHTKFTFLTEQAHTVTVLAINSI 720
Db 663 TLLWPLMKNDLSCSVQRYVINHHSTSCNGTWSVDGNGHTKFTFLTEQAHTVTVLAINSI 722
QY 721 GASVANFNLTFSWPMKYNIVQSLSAYPLNCSCTVSVWILSPSDYKMLYFIEWKNLNED 780
Db 723 GASVANFNLTFSWPMKYNIVQSLSAYPLNCSCTVSVWILSPSDYKMLYFIEWKNLNED 782
QY 781 GEIKWLRISSSVKYYIHGKF 801
Db 783 GEIKWLRISSSVKYYIHDF 803

RESULT 10
US-08-640-389A-11

; Sequence 11, Application US/08640389A
; Patent No. 5912123

GENERAL INFORMATION:

; APPLICANT: Snodgrass, H. R.

; APPLICANT: Clotfi, Joseph

; APPLICANT: Zupancic, Thomas J.

; APPLICANT: Shafer, Alan W.

; TITLE OF INVENTION: DETECTION OF THE LEPTIN

; TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR

; TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/640,389A
; FILING DATE: 29-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNTE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-640-389A-11

Query Match 98.8%; Score 4309; DB 2; Length 1165;
Best Local Similarity 99.1%; Pred. No. 0;

Matches 794; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEIYVITAFNLSPITPWRFKLSCMPPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEIYVITAFNLSPITPWRFKLSCMPPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHETAVEPEKFNSSGTHFNSLKHATFHCCFRSEQDRNCSLCADNIEGRTFVSTVNSLVF 120
Db 61 NGHETAVEPEKFNSSGTHFNSLKHATFHCCFRSEQDRNCSLCADNIEGRTFVSTVNSLVF 120
QY 121 QOIDANNIOCLWKGDLKLFICVYESLFKRLFRNYKVHLLVYLPEVLEDSPLVPQKGS 180
Db 121 QOIDANNIOCLWKGDLKLFICVYESLFKRLFRNYKVHLLVYLPEVLEDSPLVPQKGS 180
QY 181 FQVHCNCSVHECCCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPMLSVQPINNVKPDPP 240
Db 181 FQVHCNCSVHECCCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPMLSVQPINNVKPDPP 240
QY 241 LGLHMETDDGNLKISWSSPPLVPFPLOQVQKYSNSTTVIRADKIVSATSLLVDSILP 300
Db 241 LGLHMETDDGNLKISWSSPPLVPFPLOQVQKYSNSTTVIRADKIVSATSLLVDSILP 300
QY 301 GSSYEVOVGRKRLDGGCGIWSGWTSPVFTTQDVVYPPPKILTSGVSNVSHFCIYKKNKI 360
Db 301 GSSYEVOVGRKRLDGGCGIWSGWTSPVFTTQDVVYPPPKILTSGVSNVSHFCIYKKNKI 360
QY 361 VPSKEIVWMNLAEKIPQSOYDVVSDHVSQVTFNLFNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIVWMNLAEKIPQSOYDVVSDHVSQVTFNLFNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNIINISCTDGYLTMTKRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIH 480
Db 421 RYAEIYVIDVNIINISCTDGYLTMTKRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIH 480
QY 481 PISEPKDCYLOSDGFEYECIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLOSDGFEYECIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKNYEVYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKNYEVYDAKSKSVSLPV 600
QY 601 POLCAVAVQVRCRDLGGLGYWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNY 660
Db 601 POLCAVAVQVRCRDLGGLGYWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNY 660

QY 661 TLLWKPLMKNDLSCVQRYVINHTSCNGTWSGVDGNHKTFLWTEQAHVTVLAINSI 720
 DB 661 TLLWKPLMKNDLSCVQRYVINHTSCNGTWSGVDGNHKTFLWTEQAHVTVLAINSI 720
 QY 721 GASVANFNLTFSPMKSVMKNIVQSLAYPLNASSCVIVSWILSPSDYKIMVFIIEKNLNE 780
 DB 721 GASVANFNLTFSPMKSVMKNIVQSLAYPLNASSCVIVSWILSPSDYKIMVFIIEKNLNE 780
 QY 781 GEIKWLRISSSVKYYIHGKF 801
 DB 781 GEIKWLRISSSVKYYIHDF 801

RESULT 11

US-08-640-389A-10
 ; Sequence 10, Application US/08640389A
 ; Patent No. 5912123

GENERAL INFORMATION:

APPLICANT: Snodgrass, H. R.
 APPLICANT: Cioffi, Joseph
 APPLICANT: Zupancic, Thomas J.
 APPLICANT: Shafer, Alan W.

TITLE OF INVENTION: DETECTION OF THE LEPTIN

TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR

TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/640,389A

FILING DATE: 29-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Poissant, Brian M.

REGISTRATION NUMBER: 28,462

REFERENCE/DOCKET NUMBER: 8907-032

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 896 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-640-389A-10

Query Match 98.5%; Score 4297; DB 2; Length 896;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 791; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFYIYTAFLNLSYPTIPWFKLSMPNPNSTYDFLLPAGLSKNTSNS 60
 DB 1 MICQKFCVLLHWEFYIYTAFLNLSYPTIPWFKLSMPNPNSTYDFLLPAGLSKNTSNS 60
 QY 61 NGHYETAVEPKFNSSGTHFNSLSKTHFCCFRSEQRNCSLCAADNIEGKTFVSTVNSLVF 120
 DB 61 NGHYETAVEPKFNSSGTHFNSLSKTHFCCFRSEQRNCSLCAADNIEGKTFVSTVNSLVF 120
 QY 121 QQIDANWNIQCWLKGLKLFICYVESLFKNLFRNYKVHLLYVLPVLEDSPLVPQKGS 180

DB 121 QQIDANWNIQCWLKGLKLFICYVESLFKNLFRNYKVHLLYVLPVLEDSPLVPQKGS 180
 QY 181 FQWVHCNCSVHECCCLVPVPTAKLNDTLMLCKLITSGGVIFQSPLMSVQPINWVKPDP 240
 DB 181 FQWVHCNCSVHECCCLVPVPTAKLNDTLMLCKLITSGGVIFQSPLMSVQPINWVKPDP 240
 QY 241 LGHMEITDDGNLKISWSPPPLVPFPLOQYQVYSENSTTVIREADKIVSATSLLVDSILP 300
 DB 241 LGHMETTDDGNLKISWSPPPLVPFPLOQYQVYSENSTTVIREADKIVSATSLLVDSILP 300
 QY 301 GSSYEVOVRGKRLDGGIWSDSSTPRVFTTQDVIYPPPKILTSVGSNWSFHCIIYKENKI 360
 DB 301 GSSYEVOVRGKRLDGGIWSDSSTPRVFTTQDVIYPPPKILTSVGSNWSFHCIIYKENKI 360
 QY 361 VPSKETVMMNLAELKIPQSOYDVVSDHVSQVTFNFNLNETKPRGKFTYDAVYCCNEHECHH 420
 DB 361 VPSKETVMMNLAELKIPQSOYDVVSDHVSQVTFNFNLNETKPRGKFTYDAVYCCNEHECHH 420
 QY 421 RYAEYVIDVNNINISCTDGYLTMTCTRWSTSTIOSLAESTLQRLYHRSSLYCSDIPSTH 480
 DB 421 RYAEYVIDVNNINISCTDGYLTMTCTRWSTSTIOSLAESTLQRLYHRSSLYCSDIPSTH 480
 QY 481 PISEPKDCYLQSDGFEYECIFQPIFLLSGYTMIRINHSLSGSDSPPTCVLPDSVVKPLPP 540
 DB 481 PISEPKDCYLQSDGFEYECIFQPIFLLSGYTMIRINHSLSGSDSPPTCVLPDSVVKPLPP 540
 QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGREVQWKMYEVDKSKSVSLPV 600
 DB 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGREVQWKMYEVDKSKSVSLPV 600
 QY 601 PDLACVAVQVRCRDLGLGYWSNMSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKKNV 660
 DB 601 PDLACVAVQVRCRDLGLGYWSNMSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKKNV 660
 QY 661 TLLWKPLMKNDLSCVQRYVINHTSCNGTWSGVDGNHKTFLWTEQAHVTVLAINSI 720
 DB 661 TLLWKPLMKNDLSCVQRYVINHTSCNGTWSGVDGNHKTFLWTEQAHVTVLAINSI 720
 QY 721 GASVANFNLTFSPMKSVMKNIVQSLAYPLNASSCVIVSWILSPSDYKIMVFIIEKNLNE 780
 DB 721 GASVANFNLTFSPMKSVMKNIVQSLAYPLNASSCVIVSWILSPSDYKIMVFIIEKNLNE 780
 QY 781 GEIKWLRISSSVKYYIHGKF 801
 DB 781 GEIKWLRISSSVKYYIHDF 801

RESULT 12

US-08-640-389A-9
 ; Sequence 9, Application US/08640389A
 ; Patent No. 5912123

GENERAL INFORMATION:

APPLICANT: Snodgrass, H. R.

APPLICANT: Cioffi, Joseph

APPLICANT: Zupancic, Thomas J.

APPLICANT: Shafer, Alan W.

TITLE OF INVENTION: DETECTION OF THE LEPTIN

TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR

TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/640,389A
;; FILING DATE: 29-APR-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Poissant, Brian M.
;; REGISTRATION NUMBER: 28,462
;; REFERENCE/DOCKET NUMBER: 8907-032
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 906 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-08-640-389A-9

Query Match 98.5%; Score 4297; DB 2; Length 906;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 791; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPTIPWREKLSKMPNSTYDYFLLPAGLSKNTNS 60
DB 1 MICQKFCVLLHWEFIYVITAFNLSYPTIPWREKLSKMPNSTYDYFLLPAGLSKNTNS 60
QY 61 NGHETAVEPKFNSSGTHFNSLKTTHCCFRSEQRNCSLCADNIEGKTVSTVNSLVF 120
DB 61 NGHETAVEPKFNSSGTHFNSLKTTHCCFRSEQRNCSLCADNIEGKTVSTVNSLVF 120
QY 121 QQIDANNWIOCLWGLKGLFICYVESLKNFRNFKVHLLYVLPVLEDSPLVPQKGS 180
DB 121 QQIDANNWIOCLWGLKGLFICYVESLKNFRNFKVHLLYVLPVLEDSPLVPQKGS 180
QY 181 FQVHCNCSVHECCLECLVPPTAKNDTLLMCLKITSGGVIFQSPMSVQPINNVKPDPP 240
DB 181 FQVHCNCSVHECCLECLVPPTAKNDTLLMCLKITSGGVIFQSPMSVQPINNVKPDPP 240
QY 241 LGLHMETDGNLAKISSPPLPFPFQYQVKSSENSTTVTREADKIVSATSLVDSILP 300
DB 241 LGLHMETDGNLAKISSPPLPFPFQYQVKSSENSTTVTREADKIVSATSLVDSILP 300
QY 301 GSSYEVOVRKRLDGPISDWSPTPRVFTTQDVYFPPKILTSVGSNVSPHCYKKNKI 360
DB 301 GSSYEVOVRKRLDGPISDWSPTPRVFTTQDVYFPPKILTSVGSNVSPHCYKKNKI 360
QY 361 VPSKEIYVWNNLAEKIPQSDYVSDHVSQVTFNLAETPRGKFTYDAVYCNEHECHH 420
DB 361 VPSKEIYVWNNLAEKIPQSDYVSDHVSQVTFNLAETPRGKFTYDAVYCNEHECHH 420
QY 421 RYAEIYVIDNINISCTDGLTKMTCRWSTSTIOSLAESTLQLRHRSLSYCDIPSIIH 480
DB 421 RYAEIYVIDNINISCTDGLTKMTCRWSTSTIOSLAESTLQLRHRSLSYCDIPSIIH 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTWMIRINHSGLSDSPPTCVLPDSVVKPLPP 540
DB 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTWMIRINHSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKVPENNLOQIRYGLSGKEVQNMKEVYDAKSKSVSLPV 600
DB 541 SSVKAEITINIGLLKISWEKVPENNLOQIRYGLSGKEVQNMKEVYDAKSKSVSLPV 600
QY 601 PDLCAVAVOVRKRLDGLGYWNSNPATVYMDLKVPMRGPEFWRINGDTMKEKNV 660
DB 601 PDLCAVAVOVRKRLDGLGYWNSNPATVYMDLKVPMRGPEFWRINGDTMKEKNV 660
QY 661 TLLWKKPLMKNDLSLCSVQRYVINHTSCNGTWSBDVGNHTKFTFLWTEQAHTVTVLAINSI 720
DB 661 TLLWKKPLMKNDLSLCSVQRYVINHTSCNGTWSBDVGNHTKFTFLWTEQAHTVTVLAINSI 720

QY 721 GASVANFNLTFSWPMKYNIVQSLSAYPLNNSCVIVSWILSPSDYKLYFIEMKNLNE 780
DB 721 GASVANFNLTFSWPMKYNIVQSLSAYPLNNSCVIVSWILSPSDYKLYFIEMKNLNE 780
QY 781 GEIKWLRISSSVKYYIHGKF 801
DB 781 GEIKWLRISSSVKYYIHGKF 801

RESULT 13
US-08-640-389A-8
; Sequence 8, Application US/08640389A
; Patent No. 5912123
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cloffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: DETECTION OF THE LEPTIN
; TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR
; TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: - IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 29-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 958 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-640-389A-8

Query Match 98.5%; Score 4297; DB 2; Length 958;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 791; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPTIPWREKLSKMPNSTYDYFLLPAGLSKNTNS 60
DB 1 MICQKFCVLLHWEFIYVITAFNLSYPTIPWREKLSKMPNSTYDYFLLPAGLSKNTNS 60
QY 61 NGHETAVEPKFNSSGTHFNSLKTTHCCFRSEQRNCSLCADNIEGKTVSTVNSLVF 120
DB 61 NGHETAVEPKFNSSGTHFNSLKTTHCCFRSEQRNCSLCADNIEGKTVSTVNSLVF 120
QY 121 QQIDANNWIOCLWGLKGLFICYVESLKNFRNFKVHLLYVLPVLEDSPLVPQKGS 180
DB 121 QQIDANNWIOCLWGLKGLFICYVESLKNFRNFKVHLLYVLPVLEDSPLVPQKGS 180

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QY 181 FQVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGGVIFQSPMLSVQPINNVKPDPP 240
Db 181 FQVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGGVIFRSPMLSVQPINNVKPDPP 240
QY 241 LGLHMETDGNLKIWSPPPLVPFPLOQVQKYSNSTTVIREADKIVSATSLLVDSILP 300
Db 241 LGLHMETDGNLKIWSPPPLVPFPLOQVQKYSNSTTVIREADKIVSATSLLVDSILP 300
QY 301 GSSYEVOVRGKRLDGPVGSINSDNSTPRVFTTQDVYPPPKILTSGVSNVGFHCYKKNKI 360
Db 301 GSSYEVOVRGKRLDGPVGSINSDNSTPRVFTTQDVYPPPKILTSGVSNVGFHCYKKNKI 360
QY 361 VPSKEIVMNMNLAEKIPQSOYDVVSHVSKVTFNENETKPRGKFTYDVCYCCNEHCHH 420
Db 361 VPSKEIVMNMNLAEKIPQSOYDVVSHVSKVTFNENETKPRGKFTYDVCYCCNEHCHH 420
QY 421 RYAEYLVIDVNIINISCTDGYLTMTKCRWSTSTIOSLAESTLQRYHRSLSYCDIPSIH 480
Db 421 RYAEYLVIDVNIINISCTDGYLTMTKCRWSTSTIOSLAESTLQRYHRSLSYCDIPSIH 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITNIGLLKISWEKPVPEPENNLOFQIRYGLSGKEVQKMYEYVDAKSKVSLPV 600
Db 541 SSVKAEITNIGLLKISWEKPVPEPENNLOFQIRYGLSGKEVQKMYEYVDAKSKVSLPV 600
QY 601 POLCAYAVQVRCKRLDGLGYSNWSNPAYTVVMDIKVPMRGPEFWRINGDPMKKEKNV 660
Db 601 POLCAYAVQVRCKRLDGLGYSNWSNPAYTVVMDIKVPMRGPEFWRINGDPMKKEKNV 660
QY 661 TLLWPKLMDKNDLSQVQRYVINHHTSCNGTWSVDGNHKTFTFLWTEQARTVTVLAINSI 720
Db 661 TLLWPKLMDKNDLSQVQRYVINHHTSCNGTWSVDGNHKTFTFLWTEQARTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSNVIVOSLSAYPLNSCVIVSWILSPDYKLMYFIEWKNLND 780
Db 721 GASVANFNLTFSWPMKSNVIVOSLSAYPLNSCVIVSWILSPDYKLMYFIEWKNLND 780
QY 781 GEIKWLRISSVKKYYIHGKF 801
Db 781 GEIKWLRISSVKKYYIHDF 801

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RESULT 14

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US-08-640-389A-12
; Sequence 12, Application US/08640389A
; Patent No. 5912123
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Clouff, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: DETECTION OF THE LEPTIN
; TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR
; TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/640,389A
; FILING DATE: 29-APR-1996

```

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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 896 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-640-389A-12

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Query Match 77.0%; Score 3361; DB 2; Length 896;

Best Local Similarity 76.2%; Pred. No. 1.2e-299;

Matches 610; Conservative 72; Mismatches 119; Indels 0; Gaps 0;

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QY 1 MICOKFCVVLLHWEFTYVITAFNLSTYPTWPKLSCMPNPNSTYDFLLPAGLSKNTSNS 60
Db 1 MICOKFCVVLLHWEFTYVITAFNLSTYPTWPKLSCMPNPNSTYDFLLPAGLSKNTSNS 60
QY 61 NGHETAVTAPKPKNSGCTHFSNLKSTTFHCCEFRSEQDRNCSLACADNIEGKTFSTVNSLVF 120
Db 61 KGASEAIVPEKFNSSSEIYVNLKSEHCCFENEQONCSALTDTNTEGKTLASVVKASVF 120
QY 121 QOIDANWNTQWLGKDLKFLICYVESLFLPNLFRNYKVVHLLVLPDEVLEDSPLVPQKGS 180
Db 121 ROLGVNMDIECMKGDKLTICHMPLRPNFKNYDSKVHLLYDLPEVDDSDPLPKDS 180
QY 181 FQVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGGVIFQSPMLSVQPINNVKPDPP 240
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Db 241 LGLHMETDGNLKIWSPPPLVPFPLOQVQKYSNSTTVIREADKIVSATSLLVDSILP 300
QY 301 GSSYEVOVRGKRLDGPVGSINSDNSTPRVFTTQDVYPPPKILTSGVSNVGFHCYKKNKI 360
Db 301 GSSYEVOVRGKRLDGPVGSINSDNSTPRVFTTQDVYPPPKILTSGVSNVGFHCYKKNKI 360
QY 361 VPSKEIVMNMNLAEKIPQSOYDVVSHVSKVTFNENETKPRGKFTYDVCYCCNEHCHH 420
Db 361 VPSKEIVMNMNLAEKIPQSOYDVVSHVSKVTFNENETKPRGKFTYDVCYCCNEHCHH 420
QY 421 RYAEYLVIDVNIINISCTDGYLTMTKCRWSTSTIOSLAESTLQRYHRSLSYCDIPSIH 480
Db 421 RYAEYLVIDVNIINISCTDGYLTMTKCRWSTSTIOSLAESTLQRYHRSLSYCDIPSIH 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITNIGLLKISWEKPVPEPENNLOFQIRYGLSGKEVQKMYEYVDAKSKVSLPV 600
Db 541 SSVKAEITNIGLLKISWEKPVPEPENNLOFQIRYGLSGKEVQKMYEYVDAKSKVSLPV 600
QY 601 POLCAYAVQVRCKRLDGLGYSNWSNPAYTVVMDIKVPMRGPEFWRINGDPMKKEKNV 660
Db 601 POLCAYAVQVRCKRLDGLGYSNWSNPAYTVVMDIKVPMRGPEFWRINGDPMKKEKNV 660
QY 661 TLLWPKLMDKNDLSQVQRYVINHHTSCNGTWSVDGNHKTFTFLWTEQARTVTVLAINSI 720
Db 661 TLLWPKLMDKNDLSQVQRYVINHHTSCNGTWSVDGNHKTFTFLWTEQARTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSNVIVOSLSAYPLNSCVIVSWILSPDYKLMYFIEWKNLND 780
Db 721 GASVANFNLTFSWPMKSNVIVOSLSAYPLNSCVIVSWILSPDYKLMYFIEWKNLND 780

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Db 721 GASLVNLTFSWPMKSVSAVESLSAVPLSSCVLSWTLSPPDDYSLLYLVIEWKILNED 780

QY 781 GEIKWLRISSSVKYYIHGKF 801
Db 781 DGMKWLRIPSNVKFKYIHDF 801

RESULT 15
US-08-599-455B-2
Sequence 2, Application US/08599455B
Patent No. 5972621
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
MODULATE BODY WEIGHT USING THE OB RECEPTOR
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,455B
FILING DATE: 22-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Melklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/017001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-599-455B-2

Query Match 76.7%; Score 3345; DB 2; Length 894;
Best Local Similarity 76.0%; Pred. No. 3.6e-298;
Matches 609; Conservative 73; Mismatches 117; Indels 2; Gaps 2;

QY 1 MICOKFCVLLHWEFIYVITAFNLSPITPWRKLCMPNPNSTYDVFLLPAGLSKNTSNS 60
Db 1 MICOKFCVLLHWEFIYVITAFNLSPITPWRKLCMPNPNSTYDVFLLPAGLSKNTSNS 60

QY 61 NGHYETAVERKFNSSGTHFNLSKTTFTHCCFRSEQDRNCSLCADNIEGRTFVSTVNSLVF 120
Db 61 KGASEAIVEAKFNSSGIIYVPELSKTVFHCCFGNEQGCNSALTNDTNEGKTLASVVKASVF 120

QY 121 QQIDANNIOCLWGLKLFICYVESLFPKLNPNYKVVHLLVYLPVLEDSPLVPQKGS 180
Db 121 ROLGVNWDIECHWKGLDLEFICHMEPLPRNPKNYDSKVHLLYDLPEVDDSPPLPKDS 180

QY 181 FOMVHCNSVHECCCLVPVPTAKLMDTLMLCKITSGGVIFQSPLMSVQPINMVKPDP 240
Db 181 FOTVOCNCSLRG-CECHVPVPRAKLYALLMVLKLETSAGVSFQSPMLSLQPMVVKPDP 239

QY 241 LGLHMEITDDGNLKISWSPPPLPQVQVYSENSTVIREADKIVSATSLLVDSILP 300
Db 241 LGLHMEITDDGNLKISWSPPPLPQVQVYSENSTVIREADKIVSATSLLVDSILP 300

QY 301 GSSYEYQVGRKLDGPGIWSMDSTPRVFTQDVIYFPFKILTSGVSNVSHFCIYKKNKI 360
Db 299 GSSYEYQVGRKLDGPGIWSMDSTPRVFTQDVIYFPFKILTSGVSNVSHFCIYKKNKI 358

QY 361 VPSKEIVVMNLAEKIPQSDYDVSDHVSQVTFNMLNETKPRGFTYDAVYCCNEHECH 420
Db 359 TSSKOIVVMNLAEKIPQSDYDVSDHVSQVTFNMLNETKPRGFTYDAVYCCNEHECH 418

QY 421 RYAEIYVIVDYNINISCTDGYLTMTCTWSPSTIOSLGVSTVQLRYHRRSLYCPDSPSIH 478
Db 419 RYAEIYVIVDYNINISCTDGYLTMTCTWSPSTIOSLGVSTVQLRYHRRSLYCPDSPSIH 478

QY 481 PISEPKCYLQSDGFEYECIFQIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
Db 479 PTSEPKNCVLRQDGFYECVFPQIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 538

QY 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSGKEVQWKMVEYDADKSKSVSLPV 600
Db 539 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSGKEVQWKMVEYDADKSKSVSLPV 598

QY 601 PDLCAVAVQVRCRDLGLGYWSNKNSPAYTVVMDIKVPMRGPPEWRLINGDTMKKKNV 660
Db 599 PDLCAVAVQVRCRDLGLGYWSNKNSPAYTVVMDIKVPMRGPPEWRLINGDTMKKKNV 658

QY 661 TLLMKPLMKNDSLCSVQRYVINHTSCNGTWSVDYGNHTKFTFLWTEQAHVTVVLAINSI 720
Db 659 TLLMKPLMKNDSLCSVQRYVINHTSCNGTWSVDYGNHTKFTFLWTEQAHVTVVLAINSI 718

QY 721 GASVANENLTFSWPMKSVNIVQSLSPNLSAIVSPLSSCVLSWTLSPPDDYSLLYLVIEWKILNED 780
Db 719 GASVANENLTFSWPMKSVNIVQSLSPNLSAIVSPLSSCVLSWTLSPPDDYSLLYLVIEWKILNED 778

QY 781 GEIKWLRISSSVKYYIHGKF 801
Db 779 DGMKWLRIPSNVKFKYIHDF 799

Search completed: October 22, 2001, 16:05:22
Job time: 92 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 22, 2001, 16:05:01 ; Search time 31.06 Seconds

(without alignments)
3424.766 Million cell updates/sec

Title: US-09-116-676-10

Perfect score: 4363

Sequence: 1 MICQKFCVLLHWEFIIVIT.....WLRISSSVKYIYHCKFTIL 804

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_16:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_rodent:
12: sp_unclassified:
13: sp_invertebrate:
14: sp_virus:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4337	99.4	896	Q92919	Q92919 homo sapien
2	4337	99.4	958	Q92920	Q92920 homo sapien
3	4337	99.4	1165	Q92921	Q92921 homo sapien
4	4325	99.1	896	Q13594	Q13594 homo sapien
5	4325	99.1	906	Q13593	Q13593 homo sapien
6	4325	99.1	958	Q13592	Q13592 homo sapien
7	4125	94.5	894	Q9MYL1	Q9MYL1 macaca mula
8	4125	94.5	925	Q9MYK9	Q9MYK9 macaca mula
9	4125	94.5	1163	Q9MYL2	Q9MYL2 macaca mula
10	4125	94.5	1194	Q9MYL0	Q9MYL0 macaca mula
11	3711	85.1	848	Q9MZS2	Q9MZS2 sus scrofa
12	3709	85.0	1165	Q02671	Q02671 sus scrofa
13	3340	76.6	1162	Q9QWC3	Q9QWC3 mus musculus
14	3284	75.3	895	Q9DDK1	Q9DDK1 rattus norv
15	2105.5	48.3	1147	Q9IBK7	Q9IBK7 gallus gall
16	2096.5	48.1	1148	Q9IBK7	Q9IBK7 gallus gall
17	2024.5	46.4	1146	Q9IBK7	Q9IBK7 gallus gall
18	1089	25.0	246	Q35773	Q35773 rattus norv
19	683	15.7	161	Q28606	Q28606 ovis aries

20	616	14.1	147	6	Q95257	Q95257 sus scrofa
21	497	11.4	123	6	Q9NIF9	Q9NIF9 sus scrofa
22	477	10.9	121	6	O18980	O18980 bos taurus
23	456	10.5	145	13	O9IA32	O9IA32 gallus gall
24	377.5	8.7	881	13	O57519	O57519 xenopus lae
25	313.5	7.2	918	13	Q9W609	Q9W609 gallus gall
26	299	6.9	57	6	O97778	O97778 elephas max
27	299	6.9	57	6	O97778	O97778 loxodonta a
28	279	6.4	710	13	O57520	O57520 xenopus lae
29	242.5	5.6	1093	11	O70535	O70535 rattus norv
30	220	5.0	2302	11	O88488	O88488 rattus norv
31	212.5	4.9	379	4	Q98650	Q98650 homo sapien
32	196.5	4.5	970	11	O88821	O88821 mus musculus
33	192	4.4	971	11	O70458	O70458 mus musculus
34	188	4.3	329	4	Q9UQ41	Q9UQ41 homo sapien
35	178	4.1	422	4	O75462	O75462 homo sapien
36	174	4.0	422	4	Q9UHS5	Q9UHS5 homo sapien
37	174.5	4.0	425	11	Q9JMS8	Q9JMS8 mus musculus
38	168.5	3.9	346	13	Q93404	Q93404 oreochromis
39	167.5	3.8	1598	4	Q9P214	Q9P214 homo sapien
40	166	3.8	1114	5	Q9VSG6	Q9VSG6 drosophila
41	163	3.7	6875	6	Q28733	Q28733 oryctolagus
42	162.5	3.7	2037	5	Q9VLS8	Q9VLS8 drosophila
43	161.5	3.7	26926	4	O10466	O10466 homo sapien
44	158.5	3.6	638	6	Q9XS21	Q9XS21 papio anub
45	158	3.6	1005	13	P79921	P79921 xenopus lae

ALIGNMENTS

RESULT 1
Q92919 ID Q92919 PRELIMINARY; PRT: 896 AA.
AC Q92919;
DT 01-FEB-1997 (TREMREL. 02, Created)
DT 01-FEB-1997 (TREMREL. 02, Last sequence update)
DT 01-MAR-2001 (TREMREL. 16, Last annotation update)
DE LEPTIN RECEPTOR.
GN DB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP Bennett B.D., Solar G.P., Yuan J.O., Mathias J., Thomas G.R.,
RA Matthews W.;
RL Curr. Biol. 6:0-0(0).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE=97215244; PubMed=9061609;
RX Luoh S.M., Di Marco F., Levin N., Armanini M., Xie M.H., Nelson C.,
Bennett G.L., Williams M., Spencer S.A., Gurney A., de Sauvage F.J.;
RT "Cloning and characterization of a human leptin receptor using a
J. Mol. Endocrinol. 18:77-85(1997).
RL EMBL; U66495; AAC07495.1;
DR EMBL; U50748; AAC23650.1;
DR HSSP; P40189; IBOU
DR InterPro; IPR001777;
DR InterPro; IPR002996;
DR InterPro; IPR003529;
DR InterPro; IPR003531;
DR Pfam; PF00041; fn3.2
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
SQ SEQUENCE 896 AA; 102489 MW; D371C7A4186DEEF3 CRC64;

Query Match 99.4%; Score 4337; DB 4; Length 896;
Best Local Similarity 99.8%; Pred. No. 0;

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Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MICQKFCVLLHWEFIYVITAFNLSPITPWRFKLSCHMPPNSTYDYFLLPAGLSKNTSNS 60
DB 1 MICQKFCVLLHWEFIYVITAFNLSPITPWRFKLSCHMPPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHYETAPEKFNSSGTHFNSLKTTHFCCFSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
DB 61 NGHYETAPEKFNSSGTHFNSLKTTHFCCFSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QOIDANNIQCWLKGLDLKLFICYVESLEKFNFRNYKVHLLYVLPVLEDSPLVPQKGS 180
DB 121 QOIDANNIQCWLKGLDLKLFICYVESLEKFNFRNYKVHLLYVLPVLEDSPLVPQKGS 180
QY 181 FQVHCNCSVHECCCLVPVPTAKLNDTLLMCLKTSGGVIFQSPMSVQPINNVKPDPP 240
DB 181 FQVHCNCSVHECCCLVPVPTAKLNDTLLMCLKTSGGVIFQSPMSVQPINNVKPDPP 240
QY 241 LGLHMEITDDGNLKIWSGSPPLVPPELQYQVYKYSNSTTVIREADKIVSATSLVDSILP 300
DB 241 LGLHMEITDDGNLKIWSGSPPLVPPELQYQVYKYSNSTTVIREADKIVSATSLVDSILP 300
QY 301 GSSYEVOVGRKLDGPGIWSGSPPLVPPELQYQVYKYSNSTTVIREADKIVSATSLVDSILP 360
DB 301 GSSYEVOVGRKLDGPGIWSGSPPLVPPELQYQVYKYSNSTTVIREADKIVSATSLVDSILP 360
QY 361 VPSKEIIVMMNLAEKIPQSOYDVVSDHVSQVYKYSNSTTVIREADKIVSATSLVDSILP 420
DB 361 VPSKEIIVMMNLAEKIPQSOYDVVSDHVSQVYKYSNSTTVIREADKIVSATSLVDSILP 420
QY 421 RYAEIYVIDVNIINISCTDGYLTMTCRWSTSTQSLAESTLQRLYHRSSLYCSDIPSIIH 480
DB 421 RYAEIYVIDVNIINISCTDGYLTMTCRWSTSTQSLAESTLQRLYHRSSLYCSDIPSIIH 480
QY 481 PISEPKDCYQSDGFYECIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
DB 481 PISEPKDCYQSDGFYECIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKVPFENNLOFQIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600
DB 541 SSVKAEITINIGLLKISWEKVPFENNLOFQIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600
QY 601 PDLCAVAVQVRCRDLGLGYSWNSNPAYTVVMDIKVPMRGPEFWRININGDTMKKEKNV 660
DB 601 PDLCAVAVQVRCRDLGLGYSWNSNPAYTVVMDIKVPMRGPEFWRININGDTMKKEKNV 660
QY 661 TLWKPLMKNDLSCSVQRYVINHTSCNGTWSEDVGNHRTKFTFLWTEQAHTVTVLAINSI 720
DB 661 TLWKPLMKNDLSCSVQRYVINHTSCNGTWSEDVGNHRTKFTFLWTEQAHTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSNVIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEMKLNED 780
DB 721 GASVANFNLTFSWPMKSNVIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEMKLNED 780
QY 781 GEIKWLRISSSVKKYYIHGKF 801
DB 781 GEIKWLRISSSVKKYYIHGKF 801
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RESULT 2

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Q92920 PRELIMINARY; PRT; 958 AA.
ID Q92920
AC Q92920;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE LEPTIN RECEPTOR.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC NCBI_Metazoa; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
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RA Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,
RA Matthews W.;
RL Curr. Biol. 6:0-0(0);
DR EMBL: U66496; AB07496.1;
DR HSSP: P16471; 1BP3.
DR InterPro: IPR001777;
DR InterPro: IPR002996;
DR InterPro: IPR003529;
DR InterPro: IPR003531;
DR Pfam: PF00041; fn3.2;
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE: PS01353; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
SQ SEQUENCE 958 AA; 109392 MW; 3F65BC5A187E803A CRC64;
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Query Match 99.48; Score 4337; DB 4; Length 958;
Best Local Similarity 99.88; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB 1 MICQKFCVLLHWEFIYVITAFNLSPITPWRFKLSCHMPPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHYETAPEKFNSSGTHFNSLKTTHFCCFSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
DB 61 NGHYETAPEKFNSSGTHFNSLKTTHFCCFSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QOIDANNIQCWLKGLDLKLFICYVESLEKFNFRNYKVHLLYVLPVLEDSPLVPQKGS 180
DB 121 QOIDANNIQCWLKGLDLKLFICYVESLEKFNFRNYKVHLLYVLPVLEDSPLVPQKGS 180
QY 181 FQVHCNCSVHECCCLVPVPTAKLNDTLLMCLKTSGGVIFQSPMSVQPINNVKPDPP 240
DB 181 FQVHCNCSVHECCCLVPVPTAKLNDTLLMCLKTSGGVIFQSPMSVQPINNVKPDPP 240
QY 241 LGLHMEITDDGNLKIWSGSPPLVPPELQYQVYKYSNSTTVIREADKIVSATSLVDSILP 300
DB 241 LGLHMEITDDGNLKIWSGSPPLVPPELQYQVYKYSNSTTVIREADKIVSATSLVDSILP 300
QY 301 GSSYEVOVGRKLDGPGIWSGSPPLVPPELQYQVYKYSNSTTVIREADKIVSATSLVDSILP 360
DB 301 GSSYEVOVGRKLDGPGIWSGSPPLVPPELQYQVYKYSNSTTVIREADKIVSATSLVDSILP 360
QY 361 VPSKEIIVMMNLAEKIPQSOYDVVSDHVSQVYKYSNSTTVIREADKIVSATSLVDSILP 420
DB 361 VPSKEIIVMMNLAEKIPQSOYDVVSDHVSQVYKYSNSTTVIREADKIVSATSLVDSILP 420
QY 421 RYAEIYVIDVNIINISCTDGYLTMTCRWSTSTQSLAESTLQRLYHRSSLYCSDIPSIIH 480
DB 421 RYAEIYVIDVNIINISCTDGYLTMTCRWSTSTQSLAESTLQRLYHRSSLYCSDIPSIIH 480
QY 481 PISEPKDCYQSDGFYECIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
DB 481 PISEPKDCYQSDGFYECIFQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKVPFENNLOFQIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600
DB 541 SSVKAEITINIGLLKISWEKVPFENNLOFQIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600
QY 601 PDLCAVAVQVRCRDLGLGYSWNSNPAYTVVMDIKVPMRGPEFWRININGDTMKKEKNV 660
DB 601 PDLCAVAVQVRCRDLGLGYSWNSNPAYTVVMDIKVPMRGPEFWRININGDTMKKEKNV 660
QY 661 TLWKPLMKNDLSCSVQRYVINHTSCNGTWSEDVGNHRTKFTFLWTEQAHTVTVLAINSI 720
DB 661 TLWKPLMKNDLSCSVQRYVINHTSCNGTWSEDVGNHRTKFTFLWTEQAHTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSNVIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEMKLNED 780
DB 721 GASVANFNLTFSWPMKSNVIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEMKLNED 780
QY 781 GEIKWLRISSSVKKYYIHGKF 801
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Db 781 GEIKWLRISSVKKYIHDF 801
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RESULT 3
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AC Q92921
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE LEPTIN RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,
RA Matthews W.;
RL Curr. Biol. 6:0-0(0);
DR EMBL; U68497; AAB07497.1; -
DR HSSP; P40189; IBQU.
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003529; -
DR InterPro; IPR003531; -
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
SQ SEQUENCE 1165 AA; 132493 MW; CAA03BEAF2602D0A CRC64;

Query Match 99.4%; Score 4337; DB 4; Length 1165;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFYVITAFNLSPYTPWRFKLSKMPNSTYDFLLPAGLSKNTNS 60
Db 1 MICQKFCVLLHWEFYVITAFNLSPYTPWRFKLSKMPNSTYDFLLPAGLSKNTNS 60
|||||
QY 61 NGHETAVEPKENSSGTHFSNLKTTFHCCFRSEODRNSCLADNIEGKTFVSTVNSLVF 120
Db 61 NGHETAVEPKENSSGTHFSNLKTTFHCCFRSEODRNSCLADNIEGKTFVSTVNSLVF 120
|||||
QY 121 QOIDANWNTQCKLGDGLFCYVESLFKFLFRNYKYVHLVYLPVLEDSPLVPQKGS 180
Db 121 QOIDANWNTQCKLGDGLFCYVESLFKFLFRNYKYVHLVYLPVLEDSPLVPQKGS 180
|||||
QY 181 FQWVHCNCSVHECCCLVPVPTAKLNDTLMLCKLITSGGVIFQSPMLSVQPINVKPDP 240
Db 181 FQWVHCNCSVHECCCLVPVPTAKLNDTLMLCKLITSGGVIFQSPMLSVQPINVKPDP 240
|||||
QY 241 LGLHMEITDGNLKLISWSSPPLVPPLQYQVYKYSNSTTVIREADKIYSATSLVDLSILP 300
Db 241 LGLHMEITDGNLKLISWSSPPLVPPLQYQVYKYSNSTTVIREADKIYSATSLVDLSILP 300
|||||
QY 301 GSSYEVQVGRKLDGPGIWSDMSTPRVFTQDVYFPPKILTSVGSNYSFHCYKKNKI 360
Db 301 GSSYEVQVGRKLDGPGIWSDMSTPRVFTQDVYFPPKILTSVGSNYSFHCYKKNKI 360
|||||
QY 361 VPSKEIVWMNLAEPQSQYDVSDHVSQVTFNNLNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIVWMNLAEPQSQYDVSDHVSQVTFNNLNETKPRGKFTYDAVYCCNEHECHH 420
|||||
QY 421 RYAEIYVDVNIINISCTDGYLTMTCTRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIH 480
Db 421 RYAEIYVDVNIINISCTDGYLTMTCTRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIH 480
|||||
QY 481 PTSEPKDCYVQSDGFEVCFQPIFFLLSGYTMWIRINHSIGSLDSPTCVLPDSVVKPLPP 540
Db 481 PTSEPKDCYVQSDGFEVCFQPIFFLLSGYTMWIRINHSIGSLDSPTCVLPDSVVKPLPP 540
|||||

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QY 541 SSVKABITINIGLLKISWEKPPENNLFQIRYGLSGKEVQMKYEVYDAKSYSVLPV 600
Db 541 SSVKABITINIGLLKISWEKPPENNLFQIRYGLSGKEVQMKYEVYDAKSYSVLPV 600
|||||
QY 601 PDLCAVAVQVRCRKLGLGYNSNWPATVVMNDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVAVQVRCRKLGLGYNSNWPATVVMNDIKVPMRGPEFWRIINGDTMKKEKNV 660
|||||
QY 661 TLLWKPLMKNDLSLCSVQRYVINHTSCNGTWSDEVGNHTKFTFLMTEQAHTVTVLAINSI 720
Db 661 TLLWKPLMKNDLSLCSVQRYVINHTSCNGTWSDEVGNHTKFTFLMTEQAHTVTVLAINSI 720
|||||
QY 721 GASVANFNLTFSNPMKSNVIVOSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 780
Db 721 GASVANFNLTFSNPMKSNVIVOSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 780
|||||
QY 781 GEIKWLRISSVKKYIHGKF 801
Db 781 GEIKWLRISSVKKYIHDF 801
|||||
RESULT 4
Q13594 ID Q13594 PRELIMINARY; PRT; 896 AA.
AC Q13594
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE B219/OB RECEPTOR ISOFORM HUB219.3 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,
RA Platika D., Shodgrass H.R.;
RT "Novel B219/OB receptor isoforms: possible role of leptin in
RT hematopoiesis and reproduction.";
RL Nat. Med. 2:585-589(1996).
DR EMBL; U52914; AAC50511.1; -
DR HSSP; P40189; IBQU.
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003529; -
DR InterPro; IPR003531; -
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 896 B219/OB RECEPTOR ISOFORM HUB219.3.
SQ SEQUENCE 896 AA; 102515 MW; 73C431F8C578CD07 CRC64;

Query Match 99.1%; Score 4325; DB 4; Length 896;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFYVITAFNLSPYTPWRFKLSKMPNSTYDFLLPAGLSKNTNS 60
Db 1 MICQKFCVLLHWEFYVITAFNLSPYTPWRFKLSKMPNSTYDFLLPAGLSKNTNS 60
|||||
QY 61 NGHETAVEPKENSSGTHFSNLKTTFHCCFRSEODRNSCLADNIEGKTFVSTVNSLVF 120
Db 61 NGHETAVEPKENSSGTHFSNLKTTFHCCFRSEODRNSCLADNIEGKTFVSTVNSLVF 120
|||||
QY 121 QOIDANWNTQCKLGDGLFCYVESLFKFLFRNYKYVHLVYLPVLEDSPLVPQKGS 180
Db 121 QOIDANWNTQCKLGDGLFCYVESLFKFLFRNYKYVHLVYLPVLEDSPLVPQKGS 180
|||||

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Db 121 QQIDANNWNIQWLGDKLFCYVESLFRNLFNRYNYKVHLLYVLEVEDSLVPQKGS 180
QY 181 FQVHCNCSVHECCBCLVPVPTAKLNDTLMLCLKITSGGVIFQSPLSYQPINNVKPDPP 240
Db 181 FQVHCNCSVHECCBCLVPVPTAKLNDTLMLCLKITSGGVIFQSPLSYQPINNVKPDPP 240
QY 241 LGLHMEITDGNLKIWSGSPPLVPFPLOVQVYKYSNSTVIREADKIVSATSLLVDSILP 300
Db 241 LGLHMEITDGNLKIWSGSPPLVPFPLOVQVYKYSNSTVIREADKIVSATSLLVDSILP 300
QY 301 GSSYEYQVGRKLDGPGINSWSTPRVFTQDVIYPPKILTSVGSNVSFHCYKKNKI 360
Db 301 GSSYEYQVGRKLDGPGINSWSTPRVFTQDVIYPPKILTSVGSNVSFHCYKKNKI 360
QY 361 VPSKEIYVWNNLAEKIPQSOYQVDSHVSKVTFNNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIYVWNNLAEKIPQSOYQVDSHVSKVTFNNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNIINISCTDGYLTMTCTCRWSTSTIQSLAESTLQRLYHRSLSYCSIPSIH 480
Db 421 RYAEIYVIDVNIINISCTDGYLTMTCTCRWSTSTIQSLAESTLQRLYHRSLSYCSIPSIH 480
QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYVDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYVDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCRDLGLGYWSNNSPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCRDLGLGYWSNNSPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWKPLMKNDLSQVQRYVINHHTSCNGTWSDEYGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWKPLMKNDLSQVQRYVINHHTSCNGTWSDEYGNHTKFTFLWTEQAHTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSNVIVQSLASAYPLNSCVIVSWILSPSDYKLMFYIEWKNLNED 780
Db 721 GASVANFNLTFSWPMKSNVIVQSLASAYPLNSCVIVSWILSPSDYKLMFYIEWKNLNED 780
QY 781 GEIKWLRISSSVKRYIYIHGKF 801
Db 781 GEIKWLRISSSVKRYIYIHDF 801
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RESULT 5

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Q13593 ID Q13593 PRELIMINARY; PRT; 906 AA.
AC Q13593
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE B219/OB RECEPTOR ISOFORM HUB219.2 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=96206286; PubMed=8616721;
RA Clöff J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,
RA Platika D., Snodgrass H.R.;
RT *Novel B219/OB receptor isoforms: possible role of leptin in
RT hematopoiesis and reproduction.*;
RL Nat. Med. 2:585-589(1996).
DR EMBL: U52913; AAC50510.1;
DR HSSP: P40189; 1BQU.
DR InterPro: IPR001777;
DR InterPro: IPR002996;
DR InterPro: IPR003529;
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DR InterPro: IPR003531; -.
DR Pfam: PF00041; fn3; 2.
DR PROSITE: PS01353; HEMATOPO_REC_L_P2; UNKNOWN_1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
KW Signal.
FT CHAIN 1 21 POTENTIAL.
FT CHAIN 22 906 B219/OB RECEPTOR ISOFORM HUB219.2.
SQ SEQUENCE 906 AA; 103487 MW; 6D51126P33076626 CRC64;
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Query Match 99.1%; Score 4325; DB 4; Length 906;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEIYVITAFNLSPYTPWRFKLSCHPPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEIYVITAFNLSPYTPWRFKLSCHPPNSTYDYFLLPAGLSKNTSNS 60

QY 61 NGHETAVEPEKFNSSGTHFSNLKSTTFHCCFRSEODRNCSCADNIEGKTFVSTVNSLVF 120
Db 61 NGHETAVEPEKFNSSGTHFSNLKSTTFHCCFRSEODRNCSCADNIEGKTFVSTVNSLVF 120

QY 121 QQIDANNWNIQWLGDKLFCYVESLFRNLFNRYNYKVHLLYVLEVEDSLVPQKGS 180
Db 121 QQIDANNWNIQWLGDKLFCYVESLFRNLFNRYNYKVHLLYVLEVEDSLVPQKGS 180

QY 181 FQVHCNCSVHECCBCLVPVPTAKLNDTLMLCLKITSGGVIFQSPLSYQPINNVKPDPP 240
Db 181 FQVHCNCSVHECCBCLVPVPTAKLNDTLMLCLKITSGGVIFQSPLSYQPINNVKPDPP 240

QY 241 LGLHMEITDGNLKIWSGSPPLVPFPLOVQVYKYSNSTVIREADKIVSATSLLVDSILP 300
Db 241 LGLHMEITDGNLKIWSGSPPLVPFPLOVQVYKYSNSTVIREADKIVSATSLLVDSILP 300

QY 301 GSSYEYQVGRKLDGPGINSWSTPRVFTQDVIYPPKILTSVGSNVSFHCYKKNKI 360
Db 301 GSSYEYQVGRKLDGPGINSWSTPRVFTQDVIYPPKILTSVGSNVSFHCYKKNKI 360

QY 361 VPSKEIYVWNNLAEKIPQSOYQVDSHVSKVTFNNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIYVWNNLAEKIPQSOYQVDSHVSKVTFNNETKPRGKFTYDAVYCCNEHECHH 420

QY 421 RYAEIYVIDVNIINISCTDGYLTMTCTCRWSTSTIQSLAESTLQRLYHRSLSYCSIPSIH 480
Db 421 RYAEIYVIDVNIINISCTDGYLTMTCTCRWSTSTIQSLAESTLQRLYHRSLSYCSIPSIH 480

QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540

QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYVDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYVDAKSKSVSLPV 600

QY 601 PDLCAVYAVQVRCRDLGLGYWSNNSPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCRDLGLGYWSNNSPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660

QY 661 TLLWKPLMKNDLSQVQRYVINHHTSCNGTWSDEYGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWKPLMKNDLSQVQRYVINHHTSCNGTWSDEYGNHTKFTFLWTEQAHTVTVLAINSI 720

QY 721 GASVANFNLTFSWPMKSNVIVQSLASAYPLNSCVIVSWILSPSDYKLMFYIEWKNLNED 780
Db 721 GASVANFNLTFSWPMKSNVIVQSLASAYPLNSCVIVSWILSPSDYKLMFYIEWKNLNED 780

QY 781 GEIKWLRISSSVKRYIYIHGKF 801
Db 781 GEIKWLRISSSVKRYIYIHDF 801

RESULT 6

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Q13592.
AC Q13592 PRELIMINARY; PRT; 958 AA.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE B219/OB RECEPTOR ISOFORM HUB219.1 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=96206286; PubMed=8616721;
RA Cioffli J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,
RA Platika D., Snodgrass H.R.;
RT "Novel B219/OB receptor isoforms: possible role of leptin in
RT hematopoiesis and reproduction.";
RL Nat. Med. 2:585-589(1996).
DR EMBL: U52912; AAC50509.1; -
DR HSP: P40189; 1BQU.
DR InterPro: IPR001777; -
DR InterPro: IPR002996; -
DR InterPro: IPR003529; -
DR InterPro: IPR003531; -
DR Pfam: PF00041; fn3; 2
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
KW SIGNAL.
FT SIGNAL.
FT CHAIN.
FT CHAIN.
SQ SEQUENCE 958 AA; 109418 MW; C750E8D18428677B CRC64;

Query Match 99.1%; Score 4325; DB 4; Length 958;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MICOKFCVLLHWEFIVITAFNLSPYITPWRFKLSOMPNSYDFLLPAGLSKNTS 60
DB 1 MICOKFCVLLHWEFIVITAFNLSPYITPWRFKLSOMPNSYDFLLPAGLSKNTS 60
QY 61 NGHYTEAVEPKFNSSGTHFNLSKTTFFHCCFRSEQDRNCSLCADNIEGRTFVTSNLSVF 120
DB 61 NGHYTEAVEPKFNSSGTHFNLSKTTFFHCCFRSEQDRNCSLCADNIEGRTFVTSNLSVF 120
QY 121 QQIDANNIQCWLKGLKLFICVYESLFKFLFRNYKVKHLLVLPVLEDSPLVPQKGS 180
DB 121 QQIDANNIQCWLKGLKLFICVYESLFKFLFRNYKVKHLLVLPVLEDSPLVPQKGS 180
QY 181 FQMVHCNCSVHECCGLVPVPTAKLNDTLMLCKLITSGGVIFQSPMLSVQPINNVKPDPP 240
DB 181 FQMVHCNCSVHECCGLVPVPTAKLNDTLMLCKLITSGGVIFQSPMLSVQPINNVKPDPP 240
QY 241 LGLHMEITDGNLKIWSPPPLVPFLOQVQKYSNSTTVIREADKIVSATSLLDVSIPL 300
DB 241 LGLHMEITDGNLKIWSPPPLVPFLOQVQKYSNSTTVIREADKIVSATSLLDVSIPL 300
QY 301 GSSYEYQVRGKRLDGPVNSDWSPTVFTODVYFPKLTLSVGSNSVFHCYKKNKI 360
DB 301 GSSYEYQVRGKRLDGPVNSDWSPTVFTODVYFPKLTLSVGSNSVFHCYKKNKI 360
QY 361 VPSKEIWMNMLAEKIPQSOYQVSDRVSKVTFEFLNENKTPRGKFTYDVCYCCNEHCHH 420
DB 361 VPSKEIWMNMLAEKIPQSOYQVSDRVSKVTFEFLNENKTPRGKFTYDVCYCCNEHCHH 420
QY 421 RYAEIYVIDVNIINISCTDGLYFKMTCRWSTSTIQSLAESTLQLYHRSSLYCSDIPSIIH 480
DB 421 RYAEIYVIDVNIINISCTDGLYFKMTCRWSTSTIQSLAESTLQLYHRSSLYCSDIPSIIH 480
QY 481 PISEPKDCYLQSDGFEICFQPIFLLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKPLPP 540
DB 481 PISEPKDCYLQSDGFEICFQPIFLLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600
DB 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600
QY 601 PDLCAVAVQVRCKRLDGLGYWSNWPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
DB 601 PDLCAVAVQVRCKRLDGLGYWSNWPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWKPLMKNDLSVQRYVINHHTSCNGTWSVDGNGHTRKFTFLWTEQAHVTTVLAINSI 720
DB 661 TLLWKPLMKNDLSVQRYVINHHTSCNGTWSVDGNGHTRKFTFLWTEQAHVTTVLAINSI 720
QY 721 GASVANFNLTFSMPMSKVNITVQSLAYSAYPLNSSCVIVSWILSPDYKLMYFIEMKNLNE 780
DB 721 GASVANFNLTFSMPMSKVNITVQSLAYSAYPLNSSCVIVSWILSPDYKLMYFIEMKNLNE 780
QY 781 GEIKWLRISSSVKKYIHGKF 801
DB 781 GEIKWLRISSSVKKYIHGKF 801
PRT; 894 AA.
PRELIMINARY;
ID Q9MYL1
AC Q9MYL1
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE LEPTIN RECEPTOR SHORT ISOFORM.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciae;
OC Cercopitheciae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADIPOSE;
RX MEDLINE=98408931; PubMed=9738551;
RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
RT expression in the adipose tissue of normal, hyperinsulinemic, and type
RT 2 diabetic rhesus monkeys.";
RL Obes. Res. 6:353-360(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=ADIPOSE;
RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF25873; AAF35387.1; -
DR InterPro: IPR001777; -
DR InterPro: IPR002996; -
DR InterPro: IPR003529; -
DR InterPro: IPR003531; -
DR Pfam: PF00041; fn3; 2
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 894 AA; 102191 MW; B3CAF032238BAF9 CRC64;

Query Match 94.5%; Score 4125; DB 6; Length 894;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 762; Conservative 13; Mismatches 24; Indels 2; Gaps 1;

QY 1 MICOKFCVLLHWEFIVITAFNLSPYITPWRFKLSOMPNSYDFLLPAGLSKNTS 60
DB 1 MICOKFCVLLHWEFIVITAFNLSPYITPWRFKLSOMPNSYDFLLPAGLSKNTS 60
QY 61 NGHYTEAVEPKFNSSGTHFNLSKTTFFHCCFRSEQDRNCSLCADNIEGRTFVTSNLSVF 120
DB 61 NGHYTEAVEPKFNSSGTHFNLSKTTFFHCCFRSEQDRNCSLCADNIEGRTFVTSNLSVF 120
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Db 61 NGHYETAVE--FNSSDTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVTVNSVF 118
QY 121 QOIDANWNIQWLGKDLKLFICVYESLFKNLFRNYKYVHLLYVLEVDLSPLVPQKGS 180
Db 119 QMGANWNIQWLGKDLKLFICVYESLFKNLFRNYKYVHLLYVLEVDLSPLVPQKGS 178
QY 181 FQMVHCNCSVHECCBLVPVPTAKLNDTLLMCLKITSGGVIFOSPLMSVQPINNVKPDPP 240
Db 179 FQMVHCNCSVHECCBLVPVPTAKLNDTLLMCLKITSGGVIFOSPLMSVQPINNVKPDPP 238
QY 241 LGLHMEITDDGNLKIWSWSPPLVPFLOQYKYSNSTTVIREADKIVSATSLLVDSILP 300
Db 239 LGLHMEITDDGNLKIWSWSPPLVPFLOQYKYSNSTTVIREADKIVSATSLLVDSILP 298
QY 301 GSSYEVOVGRKLDGPGIWSDSSTPRVFTTQDVIYFPKILTSVGSNVSFHCIIYKKNKI 360
Db 299 GSSYEVOVGRKLDGPGIWSDSSTPRVFTTQDVIYFPKILTSVGSNVSFHCIIYKKNKI 358
QY 361 VPSKEIVVMNLAEKIPQSYDVSVDHVSQVTFNENETKPRGKFTYDAVYCCNEHECHH 420
Db 359 VSSKKIVVMNLAEKIPQSYDVSVDHVSQVTFNENETKPRGKFTYDAVYCCNEHECHH 418
QY 421 RYAEIYVDVNIINISCEPDTGTLTKMTCRWSTSTIOSLAESTLQRLYHRSLSLYCFDIPSII 480
Db 419 RYAEIYVDVNIINISCEPDTGTLTKMTCRWSTSTIOSLAESTLQRLYHRSLSLYCFDIPSII 478
QY 481 PISEPKDCYLOSDFGVECFIOPFILLSGYTMWIRNHSIGSLDSDPTCVLPDSVVKPLPP 540
Db 479 PISEPKDCYLOSDFGVECFIOPFILLSGYTMWIRNHSIGSLDSDPTCVLPDSVVKPLPP 538
QY 541 SSVKAEITINIGLLKISWEKVPFENNLOQFIRYGLSGKEVQWKMYEYVDKAKSVSLPV 600
Db 539 SSVKAEITINIGLLKISWEKVPFENNLOQFIRYGLSGKEVQWKMYEYVDKAKSVSLPV 598
QY 601 PDLCAVYAVQVRCKRDLGGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 599 PDLCAVYAVQVRCKRDLGGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 658
QY 661 TLLWPLKMNDSLCVSQVRYVNHHTSCNCTWSEGVNHTKFTFLATEQAHTVTVLAINSI 720
Db 659 TLLWPLKMNDSLCVSQVRYVNHHTSCNCTWSEGVNHTKFTFLATEQAHTVTVLAINSI 718
QY 721 GASVANFNLTFSWPMKSNVIVQSLAYSAYPLNSCVTVSWILSPSDYKLMFYIEWKNLNED 780
Db 719 GASVANFNLTFSWPMKSNVIVQSLAYSAYPLNSCVTVSWILSPSDYKLMFYIEWKNLNED 778
QY 781 GEIKWLRISSSVKKYIIHCKF 801
Db 779 GEIKWLRISSSVKKYIIHCKF 799

RESULT 8
Q9MYK9 PRELIMINARY; PRT; 925 AA.
AC Q9MYK9;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE LEPTIN RECEPTOR SHORT INSERT ISOFORM.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADIPOSE;
RX MEDLINE=98408931; PubMed=9738551;
RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
expression in the adipose tissue of normal, hyperinsulinemic, and type
2 diabetic rhesus monkeys.";
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RL Obes. Res. 6:353-360(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=ADIPOSE;
RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF225875; AAF35389.1;
DR InterPro: IPR001777;
DR InterPro: IPR002996;
DR InterPro: IPR003529;
DR InterPro: IPR003531;
DR Pfam: PF00041; fn3.2;
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 925 AA; 105721 MW; EC09C27EC29C5F3A CRC64;

Query Match 94.5%; Score 4125; DB 6; Length 925;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 762; Conservative 13; Mismatches 24; Indels 2; Gaps 1;

QY 1 MICQKFCVLLHWEFTYITAFNLSYPTTPWRFKLSCHMPNSTYDYFLLPAGLSKNTNS 60
Db 1 MICQKFCVLLHWEFTYITAFNLSYPTTPWRFKLSCHMPNSTYDYFLLPAGLSKNTNS 60
QY 61 NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVTVNSVF 120
Db 61 NGHYETAVE--FNSSDTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVTVNSVF 118
QY 121 QOIDANWNIQWLGKDLKLFICVYESLFKNLFRNYKYVHLLYVLEVDLSPLVPQKGS 180
Db 119 QMGANWNIQWLGKDLKLFICVYESLFKNLFRNYKYVHLLYVLEVDLSPLVPQKGS 178
QY 181 FQMVHCNCSVHECCBLVPVPTAKLNDTLLMCLKITSGGVIFOSPLMSVQPINNVKPDPP 240
Db 179 FQMVHCNCSVHECCBLVPVPTAKLNDTLLMCLKITSGGVIFOSPLMSVQPINNVKPDPP 238
QY 241 LGLHMEITDDGNLKIWSWSPPLVPFLOQYKYSNSTTVIREADKIVSATSLLVDSILP 300
Db 239 LGLHMEITDDGNLKIWSWSPPLVPFLOQYKYSNSTTVIREADKIVSATSLLVDSILP 298
QY 301 GSSYEVOVGRKLDGPGIWSDSSTPRVFTTQDVIYFPKILTSVGSNVSFHCIIYKKNKI 360
Db 299 GSSYEVOVGRKLDGPGIWSDSSTPRVFTTQDVIYFPKILTSVGSNVSFHCIIYKKNKI 358
QY 361 VPSKEIVVMNLAEKIPQSYDVSVDHVSQVTFNENETKPRGKFTYDAVYCCNEHECHH 420
Db 359 VSSKKIVVMNLAEKIPQSYDVSVDHVSQVTFNENETKPRGKFTYDAVYCCNEHECHH 418
QY 421 RYAEIYVDVNIINISCEPDTGTLTKMTCRWSTSTIOSLAESTLQRLYHRSLSLYCFDIPSII 480
Db 419 RYAEIYVDVNIINISCEPDTGTLTKMTCRWSTSTIOSLAESTLQRLYHRSLSLYCFDIPSII 478
QY 481 PISEPKDCYLOSDFGVECFIOPFILLSGYTMWIRNHSIGSLDSDPTCVLPDSVVKPLPP 540
Db 479 PISEPKDCYLOSDFGVECFIOPFILLSGYTMWIRNHSIGSLDSDPTCVLPDSVVKPLPP 538
QY 541 SSVKAEITINIGLLKISWEKVPFENNLOQFIRYGLSGKEVQWKMYEYVDKAKSVSLPV 600
Db 539 SSVKAEITINIGLLKISWEKVPFENNLOQFIRYGLSGKEVQWKMYEYVDKAKSVSLPV 598
QY 601 PDLCAVYAVQVRCKRDLGGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 599 PDLCAVYAVQVRCKRDLGGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 658
QY 661 TLLWPLKMNDSLCVSQVRYVNHHTSCNCTWSEGVNHTKFTFLATEQAHTVTVLAINSI 720
Db 659 TLLWPLKMNDSLCVSQVRYVNHHTSCNCTWSEGVNHTKFTFLATEQAHTVTVLAINSI 718
QY 721 GASVANFNLTFSWPMKSNVIVQSLAYSAYPLNSCVTVSWILSPSDYKLMFYIEWKNLNED 780
Db 719 GASVANFNLTFSWPMKSNVIVQSLAYSAYPLNSCVTVSWILSPSDYKLMFYIEWKNLNED 780
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Db 719 GASVANFNLTFSWPMKVNIVQSLAYPLNSSCVILSMILSPDYKLMYFIENKLNED 778
QY 781 GEIKWLRISSSVKKYIIRGKF 801
Db 779 GEIKWLRISSSVKKYIIRHDF 799
RESULT 9
Q9MYL2
ID Q9MYL2 PRELIMINARY; PRT; 1163 AA.
AC Q9MYL2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE LEPTIN RECEPTOR LONG FORM.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98408931; PubMed-9738551;
RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
RT expression in the adipose tissue of normal, hyperinsulinemic, and type
RL 2 diabetic rhesus monkeys.";
RN Obes. Res. 6:353-360(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AF222960; AAF34683.1;
DR InterPro: IPR001777;
DR InterPro: IPR002996;
DR InterPro: IPR003529;
DR InterPro: IPR003531;
DR Pfam: PF00041; fn3; 2.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
DR Receptor.
SQ SEQUENCE 1163 AA; 132295 MW; 6B7B89108F851895 CRC64;

Query Match 94.5%; Score 4125; DB 6; Length 1163;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 762; Conservative 13; Mismatches 24; Indels 2; Gaps 1;

QY 1 MICOKFCVLLHWEFIVITAFNLSYPTTPWRFKLSKMPNPNSTVDYFLLPAGLSKNTS 60
Db 1 MICOKFCVLLHWEFIVITAFNLSYPTTPWRFKLSKMPNPNSTVDYFLLPAGLSKNTS 60
QY 61 NGHYETAVERKFNSTGTHFNLSKTTTCHCCFRSEQRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHYETAVERKFNSTGTHFNLSKTTTCHCCFRSEQRNCSLCADNIEGKTFVSTVNSLVF 118
QY 121 QQIDANNIQCWLKGLDKLFCYVESLFKFLFNRYNKKVHLLVYLPVLEDSPLVPKGS 180
Db 121 QQIDANNIQCWLKGLDKLFCYVESLFKFLFNRYNKKVHLLVYLPVLEDSPLVPKGS 178
QY 181 FQVHCNCSVHECECLVPVPTAKLNDTLMLCKITSGVIFQSPMLSVOPINMKVPDP 240
Db 181 FQVHCNCSVHECECLVPVPTAKLNDTLMLCKITSGVIFQSPMLSVOPINMKVPDP 238
QY 241 LGLHMETTDGNLKISWSSPLVPFPFQYQVQKYSNSTTVIREADKIVSATSLIVDSILP 300
Db 241 LGLHMETTDGNLKISWSSPLVPFPFQYQVQKYSNSTTVIREADKIVSATSLIVDSILP 298
QY 301 GSSYEYQVRGKRLDGGPGIWSNDSTPRVFTTQDVIYFPFKILTSGVNSVPHCYKKNKI 360
Db 301 GSSYEYQVRGKRLDGGPGIWSNDSTPRVFTTQDVIYFPFKILTSGVNSVPHCYKKNKI 358

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QY 361 VPSKEIVWMNLAEKIPQSDYDVSQVSHVSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH 420
Db 359 VSSKIVWMNLAEKIPQSDYDVSQVSHVSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH 418
QY 421 RYAEIYVIDVNIINISCEITDGYLTKMTKRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIIH 480
Db 419 RYAEIYVIDVNIINISCEITDGYLTKMTKRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIIH 478
QY 481 PISEPKCYLQSDGFYECIFQPIFLLSGYTWIRINHSGLSDSPPTCVLPDPSVVKPLPP 540
Db 479 PISEPKCYLQSDGFYECIFQPIFLLSGYTWIRINHSGLSDSPPTCVLPDPSVVKPLPP 538
QY 541 SSVKAEITINIGLLKISWEKVEFENNLOFOIRYCLSGKEVQWKNYEVYDAKSXSVLPV 600
Db 539 SSVKAEITINIGLLKISWEKVEFENNLOFOIRYCLSGKEVQWKNYEVYDAKSXSVLPV 598
QY 601 PDLCAVAVQVRKRLDGLGYWSNPNPAYTVVMDIKVPMRGPEFWIRINGDTMKKEKNV 660
Db 599 PDLCAVAVQVRKRLDGLGYWSNPNPAYTVVMDIKVPMRGPEFWIRINGDTMKKEKNV 658
QY 661 TLLKPLMKNDLSGVORYVINHTSCNGTWSVDVGNHTKFTFLWTEQAHVTVVLAINSI 720
Db 659 TLLKPLMKNDLSGVORYVINHTSCNGTWSVDVGNHTKFTFLWTEQAHVTVVLAINSI 718
QY 721 GASVANFNLTFSWPMKVNIVQSLAYPLNSSCVILSMILSPDYKLMYFIENKLNED 780
Db 719 GASVANFNLTFSWPMKVNIVQSLAYPLNSSCVILSMILSPDYKLMYFIENKLNED 778
QY 781 GEIKWLRISSSVKKYIIRGKF 801
Db 779 GEIKWLRISSSVKKYIIRHDF 799
RESULT 10
Q9MYL2
ID Q9MYL2 PRELIMINARY; PRT; 1194 AA.
AC Q9MYL2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE LEPTIN RECEPTOR LONG INSERT ISOFORM.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-ADIPOSE;
RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
RT expression in the adipose tissue of normal, hyperinsulinemic, and type
RL 2 diabetic rhesus monkeys.";
RN Obes. Res. 6:353-360(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE-ADIPOSE;
RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AP225874; AAF35388.1;
DR InterPro: IPR001777;
DR InterPro: IPR002996;
DR InterPro: IPR003529;
DR InterPro: IPR003531;
DR Pfam: PF00041; fn3; 2.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
DR Receptor.
SQ SEQUENCE 1194 AA; 135824 MW; 76D023E659911AA9 CRC64;

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NCBI_TaxID=9823;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Hu X., Dai R., Li N., Wu C.;
RT *Expression, Detection, and Partial Cloning of Porcine Leptin Receptor
(OBR) Gene.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF167719; AAF89633.1; -
DR InterPro: IPR001777; -
DR InterPro: IPR002996; -
DR InterPro: IPR003529; -
DR InterPro: IPR003531; -
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 848 848
SQ SEQUENCE 848 AA; 96372 MW; 0C5AD3B40B278FAB CRC64;
Query Match 85.1%; Score 3711; DB 6; Length 848;
Best Local Similarity 85.9%; Pred. No. 5e-300;
Matches 684; Conservative 40; Mismatches 70; Indels 2; Gaps
QY 7 CVVLLHWEFYIVITAFNLSPYTPWRFKLSCMPNSTYDYFLLPAGLSKNTSNNGHVET 66
Db 1 CVVLLHWEFYIVITAFDLAYPTIPWKFKLSCMPNWTVD-FLLPAGLSKNTSTUNGDEA 59
QY 67 AVBPKNSSGTHFSNL-SKTTHCCFRSEQDNRNSLCADNIETGKFYSTVNSLVFOQIDA 125
Db VVEMELNSSGYTLNLSLKSTTFFCHCFWSEEDKNCVSHADNIAGRAFYSAVNSLVFOQTGA 119
QY 126 NNVIQCWLKGDILKFCYYESLFKNLFRNYKYVHLVLVLEVEDSPLVPQKGSFQNVH 185
Db NNVIQCWMKEDELKFCYNESLFKNPFKNYDLKVHLLYVLEVEGLSPLLQPKGSFQSVQ 179
QY 186 CNCVSHECCBLPVYPPTAKLDNTLLMCLKITISGGVIFOSPLMSVQPINMYKPPDPPLGLHM 245
Db NCNSARECECHVPVSAALKNTLLMYKITISGGVAHFSLMSVQPINVKPPOPPLGLHM 239
QY 246 EITDDGNLKSWSPPPLVPFPLOQYQVKYSENSTTVIREADKIIVSATSLLYSDSLPGSSYE 305
Db EITDTGNLKSWSPTLPVFQLOQYQVKYSENSTTNMRKADEIVSDTSLLYSDSLPGSSYE 299
QY 306 VQVRGRKDGPQIWSDNSTPRVTQQDIYVPPKILTSGVSNVSFHCIYKKENKIVPSKE 365
Db VQVRGRKDGPQIWSDNSTPFTTTQDIYVPPKILTSGVSNISLHCIIYKENKIVPSKE 359
QY 366 IVWNMLAEKIQSOQYDVVSDHVSQVTFPNLFNKTKPRCKFTYDAVYCNEHECHHRYAEL 425
Db IVWNMLAEKIQSOQYDVVSDHVSQVTFPNNNATKPRKFTYDAVYCNEHECHHRYAEL 419
QY 426 YVIDVNINISCTDGYLTAKMTCRNSTSIQSIAESTLQLRYHRSSLSCSDIPSHTPISEP 485
Db YVIDVNINISCTDGYLTAKMTCRNSTNAIQSLVGSTLQLRYHRSSLSCSDVPSVHIIEP 479
QY 486 KDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPTCPVLPSVVKPLPPSSVKA 545
Db KDCQLQRDGFYECIFQPIFLLSGYTMWIRINHLPLGSLDSPTCPVIPDSVVKPLPPSSVKA 539
QY 546 EITINGILLKISWEKPVPENNLOFIHYGLSGREVQKWKEYEYDAKSKSVSLPVPDLCA 605
Db EITATIGLLKISWEKPVPENNLOFIHYGLSGREVQKWKEYEYDVTDKLSTKSVLPDLCA 599
QY 606 VTAVQVRCRKLDGLGYSWNSNPATVVMYMDIKVPMRGPTEFWRIINGDTMKKEKNVTLLMK 665
Db VTAVQVRCRKLDGLGYSWNSNPATVVYDVVKVPIRGPEFWRIINDATKKERNITLLMK 659
QY 666 PLMKNDLSGVORYVINHHSTCNGTWSEDVGNHKTFTFLATEQAHTVTVLAINSIGASVA 725

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Db 660 PLMKNDLCSVRSYVXHTSRHGTWSDVGNHTKFLTEQAHSHVTVLAVNSIGASSA 719
Qy 726 NFNLTFSPMSKVNIVOSLSAYPLNSSCVIVSWILSPSKLMTYFIIWKNLNEDGEIKW 785
Db 720 NFNLTFSPMSKVNIVOSLSAYPLNSSCVGLSWLLSPSYNLMYFILEWKLILNEDHEIKW 779
Qy 786 LRISSVKKYIHKCF 801
Db 780 LRISSVKKYIHDHF 795

RESULT 12
ID 002671 PRELIMINARY; PRT; 1165 AA.
AC 002671;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE TRANSMEMBRANE LEPTIN RECEPTOR.
GN LEPR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Men T.Y., Lacroix D.A., Ruiz-Cortes Z.T., Song J.H., Palin M.-F.,
RA Murphy B.D.;
RT "Porcine leptin (Ob) receptor complete coding sequence.";
RN Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE 9722487; PubMed-9069130;
RA Ernst C.W., Kapke P.A., Yerle M., Rothschild M.F.;
RT "The leptin receptor gene (LEPR) maps to porcine chromosome 6.";
RL Mamm. Genome 8:226-226(1997).
DR EMBL; AF092422; AAC61766.1; -.
DR EMBL; U72070; AAC48707.1; -.
DR HSSP; P16471; 1BP3.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR InterPro; IPR003529; -.
DR InterPro; IPR003531; -.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Transmembrane.
SQ SEQUENCE 1165 AA; 132548 MW; 1BEB562FEA282F12 CRC64;

Query Match 85.0%; Score 3709; DB 6; Length 1165;
Best Local Similarity 85.3%; Pred. No. 1.1e-299;
Matches 684; Conservative 40; Mismatches 76; Indels 2; Gaps 2;

Qy 1 MICQKFCVLLHFEYIVTAFNLSTPTTPWRKLSKMPNSTYDFLLPAGLSKNTSNS 60
Db 1 MTCPKFVALLHFEYIVTAFNLSTPTTPWRKLSKMPNSTYDFLLPAGLSKNTSTL 59
Qy 61 NGHYETAPEKPNSSGTHFNSL-SKTFHCPSRSEDRNCGLCADNIEGKTFYVSTNSLV 119
Db 60 NGHDEAVVETELNISTYISLNSKTFHCPSRSEDRNCGLCADNIEGKTFYVSTNSLV 119
Qy 120 FOQIDANNIQCWLKGLKFLICYVESLFRNRYNYKVHLLYVLPVLEDSPLVPQKG 179
Db 120 FOQTGANNNIQCWLKGLKFLICYMESLFRNRYNYKVHLLYVLPVLEDSPLVPQKG 179
Qy 180 SFQWVHCNCSVHCCBCLVPVPTAKLNDTLMLCKLTSGGVIFQSPPLMSVQPINMYKPD 239
Db 180 SFQVQNCNSARECCBCHVPVSAKLNLYLLKLTSGGAVFHSPLMSVQPINMYKPD 239
Qy 240 PLGLHMEITDGNLKLISWSPPPLVPPLOVQVYKYSNSTVIREADKIYSATSLVDSIL 299
Db 240 PLGLHMEITDGNLKLISWSPPPLVPPLOVQVYKYSNSTVIREADKIYSATSLVDSIL 299

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Db 240 PLGLHMEITDGNLKLISWSPPPLVPPLOVQVYKYSNSTVIREADKIYSATSLVDSIL 299
Qy 300 PGSSYEVOVGRKLDGPGINSDMSTPRVFTQDVIYPPPKILTSVGSNVSFHCYKKNK 359
Db 300 PGSSYEVOVGRKLDGPGINSDMSTPRVFTQDVIYPPPKILTSVGSNVSFHCYKKNK 359
Qy 360 IVPSKEIYVWNNLAETIPQSOYDVVSDHVSQVTFNINLNETKPRGKFTYDAVYCCNEHECH 419
Db 360 IVSSKKIYVWNNLAETIPQSOYDVVSDHVSQVTFNINLNETKPRGKFTYDAVYCCNEHECH 419
Qy 420 HRYAELVIVDNNINISCTDGYLTWKTCRSTSTIQSLAESTLQLRYHRSLSYCSIPSI 479
Db 420 HRYAELVIVDNNINISCTDGYLTWKTCRSTSTIQSLAESTLQLRYHRSLSYCSIPSI 479
Qy 480 HPISPKDCYLQSDGFYECIFQPIFLISGYTMTIRINHSLSGLSDSPPTCVLPDSVYKPLP 539
Db 480 HPISPKDCYLQSDGFYECIFQPIFLISGYTMTIRINHSLSGLSDSPPTCVLPDSVYKPLP 539
Qy 540 PSSVKAETITNIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKYEVYDTKLKSTSLP 599
Db 540 PSSVKAETITNIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKYEVYDTKLKSTSLP 599
Qy 600 VPDLCAVYAVQVRCRDLGLGYNSNPNPAYTVMDIKVPMRGPEFWRIINGDTMKKEKN 659
Db 600 VPDLCAVYAVQVRCRDLGLGYNSNPNPAYTVMDIKVPMRGPEFWRIINGDTMKKEKN 659
Qy 660 VTLLWPKLMDNLSLCSVORYVINHHSTSCNTWSEDVGNHHTKFTFLMTEQAHTVTVLAINS 719
Db 660 ITLLWPKLMDNLSLCSVORYVINHHSTSCNTWSEDVGNHHTKFTFLMTEQAHTVTVLAINS 719
Qy 720 IGASVANFLTFSPMSKVNIVOSLSAYPLNSSCVIVSWILSPSKLMTYFIIWKNLNE 779
Db 720 IGASVANFLTFSPMSKVNIVOSLSAYPLNSSCVIVSWILSPSKLMTYFIIWKNLNE 779
Qy 780 DGEIKWLRISSVKKYIHKCF 801
Db 780 DHEIKWLRISSVKKYIHDHF 801

RESULT 13
Q9QWG3 PRELIMINARY; PRT; 1162 AA.
ID Q9QWG3;
AC Q9QWG3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE LEPTIN RECEPTOR B.
GN LEPRB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KK OBES; TISSUE=BRAIN, HYPOTHALAMUS;
RA Igel M., Taylor B.A., Phillips S.J., Becker W., Herberg L.,
RA Joost H.G.;
RT "Hyperleptinemia and leptin receptor variant Asp600Asn in the obese,
RT hyperinsulinemic KK mouse strain.";
RL J. Endocrinol. 21:337-345(1998).
DR EMBL; Y10296; CAA71342.1; -.
DR HSSP; P40189; 1BQU.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR InterPro; IPR003529; -.
DR InterPro; IPR003531; -.
DR Pfam; PF00041; fn3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW SMART; SM00060; FN3; 1.
FT RECEPTOR.
SQ SEQUENCE 1162 AA; 130786 MW; 541E77CBB46EC00D CRC64;

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Query Match      76.6%; Score 3340; DB 11; Length 1162;
Best Local Similarity 75.9%; Pred. No. 5.6e-269;
Matches 608; Conservative 74; Mismatches 117; Indels 2; Gaps 2;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RA Wang M.Y., Unger R.H.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U53144; AAB03088.1;
DR HSP: P40189; LBQU.
DR InterPro: IPR001777;
DR InterPro: IPR002996;
DR InterPro: IPR003529;
DR InterPro: IPR003531;
DR Pfam: PF00041; fn3; 2;
DR PROSITE: PS01353; HEMATOPO_REC_L_P2; UNKNOWN_1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
SQ SEQUENCE 895 AA; 101324 MW; 3C93F018A737CC07 CRC64;

Query Match      75.3%; Score 3284; DB 11; Length 895;
Best Local Similarity 75.0%; Pred. No. 1.8e-264;
Matches 601; Conservative 77; Mismatches 121; Indels 2; Gaps 2;

QY 1 MICQKFCVLLHWEFYIVITAFNLSPITPWRFKLSCMPNSTDYDFLLPAGLSKNTNS 60
DB 1 MICQKFCVLLHWEFYIVITAFNLSPITPWRFKLSCMPNSTDYDFLLPAGLSKNTNS 60
QY 61 NGHYETAPEKFNSSGTHFSNLSTFFHCCFRSEQDRNCSLCADNTEGKTFVTSNLSV 120
DB 61 KGASEALVEAKENSTGIYVSELSKTFHCCFNGEQGNCALTGTGTEKTLASVVKPLVF 120
QY 121 QOIDANNTQCKLGDGLKLFICYVESLFNLFRNYKYVHLLVYLVEVLEDSPLVPQKS 180
DB 121 ROLGVNMDTECNMGKDLTLFICHMEPLKPNPKNYDSKVHLLYDLVEVLEDSPLVP 180
QY 181 FQVHCNCSVHECCBLVPPVPTAKLNDTLMLCKLITSGGVIFQSPMLSVOPINNVKPDPP 240
DB 181 FQVHCNCSVHECCBLVPPVPTAKLNDTLMLCKLITSGGVIFQSPMLSVOPINNVKPDPP 240
QY 241 LGLHMEITDGNLKSWSPPPLVPFLOQVYKYSNTTIVREADKIVSATSLVDSILP 300
DB 241 LGLHMEITDGNLKSWSPPPLVPFLOQVYKYSNTTIVREADKIVSATSLVDSILP 300
QY 301 GSSYEYQVGRKRLDGPVPSVSTPVTQDVYPPPKILTSVGSNVSFHCYKKNKI 360
DB 301 GSSYEYQVGRKRLDGPVPSVSTPVTQDVYPPPKILTSVGSNVSFHCYKKNKI 360
QY 361 VPSKETVWMNLAEKIPQSOYDVVSDHVSKVTFNINLNETKPRGKFTYDVCNEHECHH 420
DB 361 VPSKETVWMNLAEKIPQSOYDVVSDHVSKVTFNINLNETKPRGKFTYDVCNEHECHH 420
QY 421 RYAEYLVIVDNINISCTDGYLTKMTCRWSTTQSLAESTLQLRVHRSLSYCDIPSIH 480
DB 421 RYAEYLVIVDNINISCTDGYLTKMTCRWSTTQSLAESTLQLRVHRSLSYCDIPSIH 480
QY 481 PISEPKDCYQSDGFEYCFQPIFLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
DB 481 PISEPKDCYQSDGFEYCFQPIFLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMEYVYDAKSKVSLPV 600
DB 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMEYVYDAKSKVSLPV 600
QY 601 PDLCAVAVQVRCRLDGLGYVSNNSNPATVYVMDIKVPMRGPEFWRIINGDTMKKENV 660
DB 601 PDLCAVAVQVRCRLDGLGYVSNNSNPATVYVMDIKVPMRGPEFWRIINGDTMKKENV 660
QY 661 TLLWPKMLKNDSLCSVQRYVYVNHHTSCNCTWSEDVGNHHTKFTFLTEQARTVTVLAINSI 720
DB 661 TLLWPKMLKNDSLCSVQRYVYVNHHTSCNCTWSEDVGNHHTKFTFLTEQARTVTVLAINSI 720
QY 721 GASVANFNLTFSWPKSKVIVOSLSNAYPLNNSCVIVSWILSPDSYKLMFTIETWKNLND 780
DB 721 GASVANFNLTFSWPKSKVIVOSLSNAYPLNNSCVIVSWILSPDSYKLMFTIETWKNLND 780
QY 781 GBKWLRISSVKKYIKGKF 801
DB 781 GBKWLRISSVKKYIKGKF 801
QY 799 DGMKWLRIPSNVKKYIHDF 799
DB 799 DGMKWLRIPSNVKKYIHDF 799

RESULT 14
Q62960
ID Q62960 PRELIMINARY; PRT: 895 AA.
AC Q62960.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE LEPTIN RECEPTOR.
GN ROB-R.
OS Rattus norvegicus (Rat).
```



```

721 GASVANENLFTSPMPSKVNITVQSLISAYPLNUSSCVIVSWILSPDSYKLYMYFIIEWKNLND 780
!!!: !!!!!!!TSPMPSKVNITVQSLISAYPLNUSSCVIVSWILSPDSYKLYMYFIIEWKNLND 781
719 GASLVNENLFTSPMPSKVNITVQSLISAYPLNUSSCVIVSWILSPDSYKLYMYFIIEWKNLND 782
!!!: !!!!!!!TSPMPSKVNITVQSLISAYPLNUSSCVIVSWILSPDSYKLYMYFIIEWKNLND 783
QY 781 GEIKWLRISSVKKYITHGKF 801
:!!!!!!TSPMPSKVNITVQSLISAYPLNUSSCVIVSWILSPDSYKLYMYFIIEWKNLND 784
Db 779 DGHKWLRIPSNVKYYIHDF 799
:!!!!!!TSPMPSKVNITVQSLISAYPLNUSSCVIVSWILSPDSYKLYMYFIIEWKNLND 785

RESULT 15
Q9DDK1 PRELIMINARY; PRT; 1147 AA.
ID Q9DDK1
AC Q9DDK1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE LEPTIN RECEPTOR.
OS OB-R.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagridae; Meleagris.
OX NCBI_Taxid=9103;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RC Richards M.P., Poch S.M., Ashwell C.M.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RD EMBL; AF321982; A040323.1;
RW Receptor.
KW VARIANT 1133 1133 Q -> R.
SQ SEQUENCE 1147 AA; 129131 MW; 34197B7908F734F4 CRC64;

```

Qy	543	VKABITNIGLLKISWEKPVFPENNILQFQIRYGLSGKEVQMKMYEYVDARSKSVSLPVPD	602
Db	535	IKABITNDGILLAYSWANPVPFANDLLKFOIRYAVNKEELTWELYSVSTRSAVIEV-Q	593
Qy	603	LCAYAVQVRCKRLDGLGYNSNNSPAYTVVMDDIKYPMRGPEPWIRTINGDTMKKKNVTL	662
Db	594	LCVEYIVQIRCALDGLGYNSNRSYAAVRDQAPLHGPEPWIRITEDPATGQKNVTL	653
Qy	663	LWPLPMKNDLCSVQRXVYINHFTSCNGTWSEDVGNHTKFTFLWTEQAHVTVTLAINSIGA	722
Db	654	LWOPLMKNHSLCSYSRVIKHOZSENTSWSEYDKGTCSCFPWTEHTHTITILAVNSIGA	713
Qy	723	SVANFNITFESPMPSKYNIVQSLGAYPLNSSCVIWSLTSPDSYKLMYFTIEMKNLNEDGE	782
Db	714	SSVYNNTLSRQMSYTNVAVOSLAPVWNSTCVILTWLTSPQIYVITSLIEMRNLNKEE	773
Qy	783	IKWLRISSKKYYIHGKFTIL	804
Db	774	MKWVRPVPNISKYYIYDHFLLI	795

Search completed: October 22, 2001, 16:08:26
Job time: 205 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 22, 2001, 16:04:36 ; Search time 11.98 Seconds

(without alignments)
2298.949 Million cell updates/sec

Title: US-09-116-676-10

Perfect score: 4363

Sequence: 1 MICQKFCVLLHWEFIIVIT.....WLRISSVKYYIHGKFTIL 804

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4337	99.4	1165	1	LEPR_HUMAN
2	3345	76.7	1162	1	LEPR_MOUSE
3	3342	76.6	1162	1	LEPR_RAT
4	296	6.8	917	1	IL6B_MOUSE
5	277.5	6.4	918	1	IL6B_HUMAN
6	270.5	6.2	918	1	IL6B_RAT
7	246.5	5.6	837	1	GCSR_MOUSE
8	242.5	5.6	836	1	GCSR_HUMAN
9	221.5	5.1	1097	1	LIFR_HUMAN
10	208	4.8	1092	1	LIFR_MOUSE
11	205.5	4.7	874	1	IL2S_MOUSE
12	200.5	4.6	862	1	IL2S_HUMAN
13	181	4.1	831	1	PRLR_MELGA
14	178	4.1	831	1	PRLR_CHICK
15	166.5	3.8	2029	1	LAR_DROME
16	165	3.8	630	1	PRUR_DRENI
17	158.5	3.6	462	1	IL6A_RAT
18	157	3.6	830	1	PRLR_COLLI
19	153.5	3.5	460	1	IL6A_MOUSE
20	150.5	3.4	610	1	PRLR_RAT
21	147.5	3.4	638	1	GHR_MACMU
22	145	3.3	1493	1	NEOL_MOUSE
23	143	3.3	581	1	PRUR_CEREL
24	143	3.3	638	1	GHR_HUMAN
25	142.5	3.3	1461	1	NEOL_HUMAN
26	142	3.3	1447	1	DCC_HUMAN
27	141	3.2	581	1	PRUR_BOVIN
28	141	3.2	878	1	IL3B_MOUSE
29	140.5	3.2	638	1	GHR_PIG
30	140.5	3.2	638	1	GHR_RABIT
31	140	3.2	1377	1	NEOL_RAT
32	139	3.2	635	1	TPOR_HUMAN
33	136.5	3.1	1447	1	DCC_MOUSE

34	136.5	3.1	3063	1	CAIC_HUMAN	Q99715 homo sapien
35	135.5	3.1	1013	1	EPAS_CHICK	P54755 gallus gall
36	134.5	3.1	983	1	EPAS_MOUSE	P29319 mus musculus
37	134	3.1	362	1	CNTR_CHICK	P51641 gallus gall
38	134	3.1	608	1	PRLR_MOUSE	Q08501 mus musculus
39	132.5	3.0	984	1	EPAS_RAT	Q08680 rattus norv
40	132	3.0	1897	1	PTPF_HUMAN	P10566 homo sapien
41	132	3.0	2481	1	FINC_XENLA	P191740 xenopus lae
42	131.5	3.0	622	1	PRLR_HUMAN	P16471 homo sapien
43	131.5	3.0	634	1	GHR_BOVIN	P79108 bos taurus
44	131.5	3.0	634	1	GHR_SHEEP	Q28575 ovis aries
45	131.5	3.0	1443	1	NEOL_CHICK	Q90610 gallus gall

ALIGNMENTS

RESULT 1
LEPR_HUMAN STANDARD; PRT; 1165 AA.
AC P48357;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE LEPTIN RECEPTOR PRECURSOR (LEP-R) (OB RECEPTOR) (OB-R).
GN LEPR OR OBR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RC MEDLINE=96128129; PubMed=8548812;
RA Tartaglia L.A., Dembski M., Weng X., Deng N., Culpepper J., Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J., Muir C., Sanker S., Moriarty A., Moore K.J., Smutko J.S., Mays G.G., Wolf E.A., Monroe C.A., Tepper R.I.;
RT *Identification and expression cloning of a leptin receptor, OB-R.*;
RL Cell 83:1263-1271(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX Thompson D.B., Ossowski V., Sutherland J., Apel W., Biesterfeldt J.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RX VARIANT ARG-223.
RX MEDLINE=96270489; PubMed=8666155;
RX Considine R.V., Considine E.L., Williams C.J., Hyde T.M., Caro J.F.;
RT *The hypothalamic leptin receptor in humans: identification of incidental sequence polymorphisms and absence of the db/db mouse and fa/fa rat mutations.*;
RL Diabetes 45:992-994(1996).
RN [4]
RX VARIANTS ARG-109; ARG-204; ARG-223 AND ASN-656.
RX MEDLINE=97289527; PubMed=9144432;
RX Ewald S.M., Soerensen T.D., Soerensen T.I., Tybjaerg-Hansen A., Andersen S.M., Chung W.K., Leibel R.L., Pedersen O.;
RT *Amino acid variants in the human leptin receptor: lack of association to juvenile onset obesity.*;
RL Biochem. Biophys. Res. Commun. 233:248-252(1997).
RN [5]
RX VARIANTS ARG-109; ARG-223 AND ASN-656.
RX MEDLINE=97431549; PubMed=9287054;
RX Chung W.K., Power-Kehoe L., Chua M., Chu F., Aronne L., Huma Z., Sothorn M., Udall J.N., Kahle B., Leibel R.L.;
RT *Exonic and intronic sequence variation in the human leptin receptor gene (LEPR).*;
RL Diabetes 46:1509-1511(1997).
RN [6]
RX VARIANTS ARG-109 AND ARG-223.
RX MEDLINE=97301763; PubMed=9158141;
RX Thompson D.B., Ravussin E., Bennett P.H., Bogardus C.;

RT *Structure and sequence variation at the human leptin receptor gene in
 RT lean and obese Pima Indians.*;
 RN Hum. Mol. Genet. 6:675-679(1997).
 RN (7)

RP VARIANTS ARG-109; ARG-223; ASN-656 AND THR-675.

RX MEDLINE-99075638; PubMed-9860295;

RA Roth H., Korn T., Rosenkranz K., Hinney A., Ziegler A., Kunz J.,

RA Siegfried W., Mayer H., Hebebrand J., Grzeschik K.-H.;

RT *Transmission disequilibrium and sequence variants at the leptin

RT receptor gene in extremely obese German children and adolescents.*;

RL Hum. Genet. 103:540-546(1998).
 RN (8)

RN VARIANTS ARG-109; ARG-223 AND ASN-656.

RX MEDLINE-97318795; PubMed-9175732;

RA Gotoda T., Manning B.S., Goldstone A.P., Imrie H., Evans A.L.,

RA Strosberg A.D., McKeligue P.M., Scott J., Altman T.J.;

RT *Leptin receptor gene variation and obesity: lack of association in a

RT white British male population.*;

RL Hum. Mol. Genet. 6:869-876(1997).

CC -!- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

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DR EMBL; U43168; AAB09673.1; .

DR EMBL; U59263; AAB09673.1; JOINED.

DR EMBL; U59248; AAB09673.1; JOINED.

DR EMBL; U59249; AAB09673.1; JOINED.

DR EMBL; U59250; AAB09673.1; JOINED.

DR EMBL; U59252; AAB09673.1; JOINED.

DR EMBL; U59253; AAB09673.1; JOINED.

DR EMBL; U59254; AAB09673.1; JOINED.

DR EMBL; U59255; AAB09673.1; JOINED.

DR EMBL; U59256; AAB09673.1; JOINED.

DR EMBL; U59257; AAB09673.1; JOINED.

DR EMBL; U59258; AAB09673.1; JOINED.

DR EMBL; U59259; AAB09673.1; JOINED.

DR EMBL; U59260; AAB09673.1; JOINED.

DR EMBL; U59261; AAB09673.1; JOINED.

DR EMBL; U59262; AAB09673.1; JOINED.

DR HSP; P10912; 3HHR.

DR MIM; 601007; .

DR InterPro; IPR001777; .

DR InterPro; IPR002465; .

DR Pfam; PF00041; fn3.2.

DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.

KW Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism.

FT SIGNAL 1 ? POTENTIAL.

FT CHAIN ? 1165 LEPTIN RECEPTOR.

FT DOMAIN ? 841 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 842 862 POTENTIAL.

FT DOMAIN 863 1165 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 237 320 FIBRONECTIN TYPE-III.

FT DOMAIN 537 623 FIBRONECTIN TYPE-III.

FT DOMAIN 738 823 FIBRONECTIN TYPE-III.

FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	397	397	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	433	433	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	516	516	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	624	624	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	659	659	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	670	670	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	688	688	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	697	697	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	728	728	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	750	750	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	VARIANT	109	109	K -> R.	/FTid=VAR_002703.
FT	VARIANT	204	204	K -> R.	/FTid=VAR_002704.
FT	VARIANT	223	223	Q -> R.	/FTid=VAR_002705.
FT	VARIANT	656	656	K -> N.	/FTid=VAR_002706.
FT	VARIANT	675	675	S -> T.	/FTid=VAR_002707.
SQ	SEQUENCE	1165 AA;	132449 MW;	8FF21D9AF5125808 CRC64;	

Query Match 99.4%; Score 4337; DB 1; Length 1165;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MICQKFCVLLHWEFIYVITAFNLSYPTTPWRFKLSCHMPNSTYDYFLPAGLSKNTNS	60
Db	1	MICQKFCVLLHWEFIYVITAFNLSYPTTPWRFKLSCHMPNSTYDYFLPAGLSKNTNS	60
Qy	61	NGHETAVEPKFNSGTHFNSLSKTTTHCCFRSDRCNSLCADNIEGKTFVSTVNSLVF	120
Db	61	NGHETAVEPKFNSGTHFNSLSKTTTHCCFRSDRCNSLCADNIEGKTFVSTVNSLVF	120
Qy	121	QOIDANWNIQCLWGLDLKLFICYVESLFKNLFNRYNKKVHLLYVLPVLEDSPLVPQKS	180
Db	121	QOIDANWNIQCLWGLDLKLFICYVESLFKNLFNRYNKKVHLLYVLPVLEDSPLVPQKS	180
Qy	181	FQMVHCNSVHECCCLVPVPTAKLNDTLMLCLKITSGVIFQSPPLMSVQPINNVKPDPP	240
Db	181	FQMVHCNSVHECCCLVPVPTAKLNDTLMLCLKITSGVIFQSPPLMSVQPINNVKPDPP	240
Qy	241	LGLHMETDGCNLKISWSSPPLVPFPLOQYQVYSENSTTVIREADKIVSATSLVDSLTLP	300
Db	241	LGLHMETDGCNLKISWSSPPLVPFPLOQYQVYSENSTTVIREADKIVSATSLVDSLTLP	300
Qy	301	GSSYEYQVRGKRLDGPGLWSDWSTPRVFTTQDVIFYPFKILTSGVNSVSPHCYKKNKI	360
Db	301	GSSYEYQVRGKRLDGPGLWSDWSTPRVFTTQDVIFYPFKILTSGVNSVSPHCYKKNKI	360
Qy	361	VPSKEIVWNNLAELKIPQSDYDVSDVSHVSKVTBPNLNETPRGKFTYDQVYCCNEHCCH	420
Db	361	VPSKEIVWNNLAELKIPQSDYDVSDVSHVSKVTBPNLNETPRGKFTYDQVYCCNEHCCH	420
Qy	421	RYAELYVDVNNINISCEYDGLTKMTCTWSTSTIQSLAESTLQLRHRSLSYCSIDPSIH	480
Db	421	RYAELYVDVNNINISCEYDGLTKMTCTWSTSTIQSLAESTLQLRHRSLSYCSIDPSIH	480
Qy	481	PISEPKCYLQSDGDFYECIFQPIFLLSGYTMWIRINISLGLSDSPPTCVLPDSVVKPLPP	540
Db	481	PISEPKCYLQSDGDFYECIFQPIFLLSGYTMWIRINISLGLSDSPPTCVLPDSVVKPLPP	540
Qy	541	SSVKAETITNIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV	600
Db	541	SSVKAETITNIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV	600
Qy	601	PDLCATVAVQVRCKRLDGLGWSWNSNPATVYVMDIKVPMRGPEFWRININGDTMKKEKV	660
Db	601	PDLCATVAVQVRCKRLDGLGWSWNSNPATVYVMDIKVPMRGPEFWRININGDTMKKEKV	660
Qy	661	TLWKPLMKNDLCSVQRYVINHHSTSCNGTWSEVDGHNHTFTFLWTEQAHVTVTVAINSI	720
Db	661	TLWKPLMKNDLCSVQRYVINHHSTSCNGTWSEVDGHNHTFTFLWTEQAHVTVTVAINSI	720

Db 661 TLLMKPLMKNDLCSQVRYVNHHTSCNGTWSVDVGNHKTFTLWTRQAHVTVVLAINSI 720

Qy 721 GASVANFNLTSPMPKVNIVQSLSPAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 721 GASVANFNLTSPMPKVNIVQSLSPAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 781 GEIKWLRISSSVKKYYIHGKF 801
 |||||||||||||||||||||||||||

Db 781 GEIKWLRISSSVKKYYIHDFH 801
 |||||||||||||||||||||||||||

RESULT 2

ID LEPN_MOUSE STANDARD; PRT: 1162 AA.

AC P48356; O35686; Q61215; Q64309; O54986;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE LEPN RECEPTOR PRECURSOR (LEP-R) (OB RECEPTOR) (OB-R) (B219 RECEPTOR).

DE RECEPTOR).

GN LEPN OR OBR OR DB.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RP SEQUENCE FROM N.A. (VARIANT A).

RC TISSUE=Choroid plexus;

RX MEDLINE=96128129; PubMed=8548812;

RA Tartaglia L.A., Dembski M., Weng X., Deng X., Culpepper J., Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J., Muir C., Sanker S., Moriarty A., Moore K.J., Smutko J.S., Mays G.G., Woolf E.A., Monroe C.A., Tepper R.I.;

RT "Identification and expression cloning of a leptin receptor, OB-R.;"

RL Cell 83:1263-1271(1995).

RN [2]

RP SEQUENCE FROM N.A. (VARIANT B).

RC STRAIN=C57BL/KSJ; TISSUE=Hypothalamus;

RX MEDLINE=96190816; PubMed=8606803;

RA Chen H., Charlat O., Tartaglia L.A., Woolf E.A., Weng X., Ellis S.J., Lakey N.D., Culpepper J., Moore K.J., Breitbart R.E., Duyk G.M., Tepper R.I., Morgenstern J.P.;

RT "Evidence that the diabetes gene encodes the leptin receptor: identification of a mutation in the leptin receptor gene in db/db mice.;"

RL Cell 84:491-495(1996).

RN [3]

RP SEQUENCE FROM N.A. (VARIANTS A TO E).

RC STRAIN=C57BL/KSJ; TISSUE=Hypothalamus;

RX MEDLINE=96231997; PubMed=8628397;

RA Lee G.-H., Proenca R., Montez J.M., Carroll K.M., Darvishzadeh J.G., Lee J.I., Friedman J.M.;

RT "Abnormal splicing of the leptin receptor in diabetic mice.;"

RL Nature 379:632-635(1996).

RN [4]

RP SEQUENCE FROM N.A. (VARIANT C).

RC STRAIN=BALB/C; TISSUE=Liver;

RX MEDLINE=96206286; PubMed=8616721;

RA Clouff J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A., Platika D., Snodgrass H.R.;

RT "Novel B219/OB receptor isoforms: possible role of leptin in hematopoiesis and reproduction.;"

RL Nat. Med. 2:585-589(1996).

RN [5]

RP SEQUENCE FROM N.A. (VARIANT B).

RC STRAIN=NEW ZEALAND OBESE / NZO; TISSUE=Hypothalamus;

RX MEDLINE=97462708; PubMed=9322935;

RA Igel M., Becker W., Herberg L., Joost H.G.;

RT "Hyperleptinemia, leptin resistance, and polymorphic leptin receptor in the New Zealand obese mouse.;"

RL Endocrinology 138:4234-4239(1997).

RN [6]

RP SEQUENCE FROM N.A. (VARIANTS A AND B).

RC STRAIN=FVB/N; TISSUE=Spleen;

RX MEDLINE=96270520; PubMed=8692797;

RA Ghilardi N., Ziegler S., Wiestner A., Stoffel R., Heim M.H., Skoda R.C.;

RT "Defective STAT signaling by the leptin receptor in diabetic mice.;"

RL Proc. Natl. Acad. Sci. U.S.A. 93:6231-6235(1996).

RN [7]

RP SEQUENCE FROM N.A. (VARIANT E).

RC STRAIN=129/J;

RX MEDLINE=98008913; PubMed=9344648;

RA Chua S.C., Koutiras I.K., Han L., Liu S.M., Kay J., Young S.J., Chung W.K., Leibel R.L.;

RT "Fine structure of the murine leptin receptor gene: splice site suppression is required to form two alternatively spliced transcripts.;"

RL Genomics 45:264-270(1997).

CC -1- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).

CC -1- FUNCTION: THE SHORT FORM (VARIANT A) MAY ACT TO TRANSPORT LEPTIN TO THE CEREBROSPINAL FLUID. THE PUTATIVE SOLUBLE RECEPTOR (VARIANT E) COULD FUNCTION AS A TRANSPORT PROTEIN.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXCEPT FOR FORM E WHICH COULD BE SECRETED.

CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; A, B (SHOWN HERE), C, D AND E; ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- TISSUE SPECIFICITY: (1) VARIANT A: HIGHEST LEVEL OF EXPRESSION IN LUNG AND KIDNEY, ALSO PRESENT IN CHOROID PLEXUS AND HYPOTHALAMUS. (2) VARIANT B: HIGHEST LEVEL OF EXPRESSION IN HYPOTHALAMUS AND LOWER LEVEL IN BRAIN, TESTES AND ADIPOSE TISSUE. (3) VARIANT E: EXPRESSED IN ADIPOSE TISSUE, HYPOTHALAMUS, HEART, AND TESTES.

CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

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CC EMBL: U42467; AAA93014.1;

CC EMBL: U46135; AAC52408.1;

CC EMBL: U49106; AAC52420.1;

CC EMBL: U49107; AAC52421.1;

CC EMBL: U49108; AAC52422.1;

CC EMBL: U49109; AAC52423.1;

CC EMBL: U49110; AAC52424.1;

CC EMBL: U52915; AAC52599.1;

CC EMBL: Y10298; CAAT71343.1;

CC EMBL: U58861; AAC52705.1;

CC EMBL: U58862; AAC52706.1;

CC EMBL: U58863; AAC52707.1;

CC EMBL: AF039456; AAB95334.1;

CC EMBL: AF039443; AAB95334.1; JOINED.

CC EMBL: AF039444; AAB95334.1; JOINED.

CC EMBL: AF039445; AAB95334.1; JOINED.

CC EMBL: AF039446; AAB95334.1; JOINED.

CC EMBL: AF039447; AAB95334.1; JOINED.

CC EMBL: AF039448; AAB95334.1; JOINED.

CC EMBL: AF039449; AAB95334.1; JOINED.

CC EMBL: AF039450; AAB95334.1; JOINED.

CC EMBL: AF039451; AAB95334.1; JOINED.

CC EMBL: AF039452; AAB95334.1; JOINED.

CC EMBL: AF039453; AAB95334.1; JOINED.

CC EMBL: AF039454; AAB95334.1; JOINED.

CC EMBL: AF039455; AAB95334.1; JOINED.

CC HSP; P16471; IBP3.

CC MGD; MGI:104993; Lepr.

CC InterPro; IPR001777; -.

CC InterPro; IPR002465; -.

CC Pfam; PF00041; fn3; 3.

CC PROSITE; PS01353; HEMATOPO_REC_L_P2; 1.

CC Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;

KW

RA Karlsson C., Lindell K., Robinson I.C.A.F., Carlsson L.M.S.,
 RA Carlsson B.;
 RT "Cloning of the rat leptin receptor.";
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. AND VARIANT FA PRO-269 (VARIANT A).
 RC STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY;
 RX MEDLINE-96212906; PubMed-8630068;
 RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.;
 RT "Phenotype-linked amino acid alteration in leptin receptor cDNA from
 RT Zucker fatty (fa/fa) rat.";
 RL Biochem. Biophys. Res. Commun. 222:19-26(1996).
 RN [6]
 RP SEQUENCE OF 1-123 FROM N.A.
 RA Morishita T., Hidaka T., Kuzuyama T., Noguchi T.;
 RT "Analysis of rat leptin receptor gene.";
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 694-878 FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Pancreas;
 RA Ma Z.;
 RT "Identification of a leptin receptor in islet.";
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE OF 843-892 FROM N.A. (VARIANT C).
 RC STRAIN-SPRAGUE-DAWLEY;
 RA Chien E.K., Hara M., Rouard M., Yano H., Philippe M., Polonsky K.S.,
 RA Bell G.I.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP VARIANT FA PRO-269.
 RX MEDLINE-96314329; PubMed-8690163;
 RA Chua S.C. Jr., White D.W., Wu-Peng X.S., Liu S.M., Okada N.,
 RA Kershaw E.E., Chung W.K., Power-Kehoe L., Chua M., Tartaglia L.A.,
 RA Leibel R.L.;
 RT "Phenotype of fatty due to Gln269Pro mutation in the leptin receptor
 RT (Lepr).";
 RL Diabetes 45:1141-1143(1996).
 CC -1- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).
 CC -1- FUNCTION: THE SHORT FORM (VARIANT A) MAY ACT TO TRANSPORT LEPTIN
 CC TO THE CEREBROSPINAL FLUID. THE PUTATIVE SOLUBLE RECEPTOR (VARIANT
 CC E) COULD FUNCTION AS A TRANSPORT PROTEIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXCEPT FOR FORM E
 CC WHICH COULD BE SECRETED.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; A, B (SHOWN HERE), C, D AND E;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- DISEASE: THE FATTY (FA) MUTATION PRODUCES PROFOUND OBESITY OF
 CC EARLY ONSET CAUSED BY HYPERPHAGIA, DEFECTIVE NONSHIVERING
 CC THERMOGENESIS, AND PREFERENTIAL DEPOSITION OF ENERGY INTO ADIPOSE
 CC TISSUE.
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC
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 CC
 CC -----
 CC EMBL; U52966; AAC52587.1;
 CC EMBL; D84550; BAA12697.1;
 CC EMBL; D84551; BAA12698.1;
 CC EMBL; D85557; BAA12830.1;
 CC EMBL; D85558; BAA12831.1;
 CC EMBL; D85559; BAA12832.1;
 CC EMBL; U60151; AAB06616.1;
 CC EMBL; D84125; BAA12230.1;
 CC EMBL; D84126; BAA12231.1;
 CC EMBL; AB011006; BAA24899.1;
 CC EMBL; U67207; ABA04654.1;
 CC EMBL; AF007818; AAB63201.1;
 CC
 CC -----

DR InterPro: IPR001777;
 DR InterPro: IPR002465;
 DR Pfam: PF00041; fn3; 2;
 DR PROSITE; PS01353; HEMATOPOI_REC_L_F2; 1;
 KW Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;
 RN Alternative splicing...
 FT SIGNAL 1 ?
 FT CHAIN ? 1162
 FT DOMAIN ? 839
 FT TRANSMEM 860
 FT DOMAIN 861 1162
 FT DOMAIN 236 318
 FT DOMAIN 535 621
 FT DOMAIN 736 821
 FT CARBOHYD 55 55
 FT CARBOHYD 56 56
 FT CARBOHYD 73 73
 FT CARBOHYD 98 98
 FT CARBOHYD 187 187
 FT CARBOHYD 275 275
 FT CARBOHYD 345 345
 FT CARBOHYD 356 356
 FT CARBOHYD 431 431
 FT CARBOHYD 514 514
 FT CARBOHYD 622 622
 FT CARBOHYD 657 657
 FT CARBOHYD 668 668
 FT CARBOHYD 686 686
 FT CARBOHYD 695 695
 FT CARBOHYD 698 698
 FT CARBOHYD 726 726
 FT VARSPLIC 890 894
 FT VARSPLIC 895 1162
 FT VARSPLIC 893 1162
 FT VARSPLIC 797 805
 FT VARSPLIC 806 1162
 FT VARIANT 269 269
 FT CONFLICT 2 2
 FT CONFLICT 12 12
 FT CONFLICT 34 34
 FT CONFLICT 751 752
 FT CONFLICT 846 846
 SQ SEQUENCE 1162 AA; 130832 MW; BA7AC2CA2D2E62AF CRC64;

Query Match 76.6%; Score 3342; DB 1; Length 1162;
 Best Local Similarity 76.0%; Pred. No. 1.3e-235;
 Matches 609; Conservative 74; Mismatches 116; Indels 2; Gaps 2;
 QY 1 MICQKFCVLLHWEFYIVITAFNLSPYIPFWRFKLSMPNPNSTYDYFLPLPAGLSKNTNS 60
 Db 1 MTCQKFCVLLHWEFYIVITAFNLSPYIPFWRFKLSMPNPNSTYDYFLPLPAGLSKNTNS 60
 QY 61 NGHYETAVPEKNSGTHPSNLSKTTFFHCCFRSEQRNCSLCAADNTEGKTFTVNSLVF 120
 Db 61 KGASEALVEAKENSTGIYVSELSKTTFFHCCFRSEQRNCSLCAADNTEGKTFTVNSLVF 120
 QY 121 QCIDANNTQCKLGDGLKFCYVESLFNLFNRYNYKVHLLVLPVLEDSPLVPQKGS 180
 Db 121 RQGVNMDTECNMKGDLTFLFCHMEPLLNPKFNKVDYDLPVLEDSPLVPQKGS 180
 QY 181 FQWVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGVIFQSPMSVQPTNMVKKPDP 240
 Db 181 FQVQCNCVRE-CECHVVPRAKYNVALLMYLETISAGVSFQSPMSVQPTNMVKKPDP 239
 QY 241 LGLHMEITDGNLKSWSPPPLVPFLOVQYKSENSTTVIREADKIVSATSLVDSILP 300
 Db 240 LGLRMEVTDGNLKSWSPPPLVPFLOVQYKSENSTTVIREADKIVSATSLVDSILP 298
 QY 301 GSSYEYQVGRKRLDGPDIWSDNSTPRVFTQDVIYFPFKILTSVGSNVSFHCYKKNKI 360
 Db 299 GSSYEYQVGRKRLDGPDIWSDNSTPRVFTQDVIYFPFKILTSVGSNVSFHCYKKNKI 358

Db 262 KDASTWIOVPLEDTMSPRTSFTVQDLKPFTTEVVFPRISIKSGKYSWDSSEASGTYIE 321
 QY 636 IKVPRGPEFWRINGDMWKEKNWTLWKLPMKNDKSCVORY--VINHTSCNGTWSE 693
 Db 322 DR-PSRPPSPFKYKTNPSHGOEYRSRLWIKALPLSEANGKILDEYILVTSQSKSVQTVV 380
 QY 694 DVGNHTKFTFLTEQAHTVTVLATNIGASVANFNLTFSWP-MSKVNIVQSLSAYPLNS 752
 Db 381 ---TGTETLVNTDRYVLAARKNKVGSAAV-LTIPSPHTVAAYSVWNLKAPP-KDN 435
 QY 753 CVIVSWILSPDYKLMFYIEKWNLEDGEI--KWLRISSVKKYIYHGK 800
 Db 436 LLWVEW--TPPKPKVSKYLEMVCVLSNAPCVEDQDQEDATVNRTHLGR 483

RESULT 5
 IL6B_HUMAN STANDARD; PRT; 918 AA.
 AC P40189;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
 DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130) (ONCOSTATIN M
 DE RECEPTOR) (CDW130) (CD130 ANTIGEN).
 GN IL6ST.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Myeloma, and Placenta;
 RX MEDLINE=9108484; PubMed=2261637;
 RA Hibi M., Murakami M., Saito M., Hirano T., Taga T., Kishimoto T.;
 RT "Molecular cloning and expression of an IL-6 signal transducer,
 RL gp130.";
 RL Cell 63:1149-1157(1990).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.
 RX MEDLINE=98169383; PubMed=9501088;
 RA Bravo J., Staunton D., Heath J.K., Jones E.Y.;
 RT "Crystal structure of a cytokine-binding region of gp130.";
 RL EMBO J. 17:1665-1674(1998).
 CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
 CC IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
 CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
 CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
 CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
 CC EMBRYONIC DEVELOPMENT (BY SIMILARITY).
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND IN ALL THE TISSUES AND CELL LINES
 CC EXAMINED. EXPRESSION NOT RESTRICTED TO IL-6 RESPONSIVE CELLS.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD130 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd130.htm".
 CC -----
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 CC -----
 CC EMBL; M57230; AAA59155.1; -
 CC FIR; A36337; A36337.
 CC PDB; 1BOU; 26-AUG-98.
 CC MIM; 600694; -
 CC InterPro; IPR001777; -

DR InterPro; IPR002465; -
 DR Pfam; PF00041; fn3; 3.
 DR PRINTS; PR00014; FNTYPEIII.
 DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
 KW Repeat; 3D-structure.
 FT SIGNAL 1 22
 FT CHAIN 23 918
 FT DOMAIN 23 619
 FT TRANSMEM 620 641
 FT DOMAIN 642 918
 FT DOMAIN 26 120
 FT DOMAIN 124 222
 FT DOMAIN 223 324
 FT DOMAIN 325 423
 FT DOMAIN 424 517
 FT DOMAIN 518 613
 FT DOMAIN 725 755
 FT DISULFID 134 144
 FT DISULFID 172 182
 FT CARBOHYD 43 83
 FT CARBOHYD 83 83
 FT CARBOHYD 131 131
 FT CARBOHYD 157 157
 FT CARBOHYD 227 227
 FT CARBOHYD 379 379
 FT CARBOHYD 383 383
 FT CARBOHYD 390 390
 FT CARBOHYD 553 553
 FT CARBOHYD 564 564
 FT SEQUENCE 918 AA; 103522 MW; D813F3672DD10D53 CRC64;
 Query Match 6.4%; Score 277.5; DB 1; Length 918;
 Best Local Similarity 22.7%; Pred. No. 1 6e-12;
 Matches 112; Conservative 82; Mismatches 227; Indels 73; Gaps 22;

QY 337 PKILTSVGSNSVFHCYKK---ENKIVPSKEIWMNMNLAEKIPQSQDYVSVHVSQVTF 393
 Db 33 PESPVLQHSNFTAVCVLKEKMDYFHVNAVYVWKTN-HFTIPKEQYTIINRTASSVTF 91
 QY 394 FNLNETPKRGKFFDYDAVCNNEHCHEHRYAEIVDV-----NINISC-ETDGLTK 444
 Db 92 TDI-----ASLNTQLTCNLTFCLEQNVYGITIISGLPPEKPKNLSVNEG--KK 141
 QY 445 MTCRWSTTIOSLAESTLQRLRYHRSLYCSDFSIHPISPEKDCYLQSDGFYECI--FQP 502
 Db 142 MRCWEGG-----REHLENTNFTLKSEWAT-----HKFA---DCKARDPPTCTVDYST 188
 QY 503 IFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVYVKPLPPSSVKAETIN----IGLLKISW 558
 Db 189 VYEVN-IEYVVEAENALGKVTSDHINFDPYVKVKNPPHNL---VINSEELSKLITW 244
 QY 559 EKP-----VFPENNLQFQRYGLSGREVKQMYEVYDAKSKSVLPVPLD--CAVYAVQV 611
 Db 245 TNPISKSVILKYNIQYTKDAST-----WSQIPPEDTASTRSFTVQDLKPFTEVFRI 299
 QY 612 RCKRLDGLGVSNWNSPAYTVVMDIKVPRGPEFWRLINGDTHMKKEKNVTLWKPLMKND 671
 Db 300 RCKMDGKGWSDWSEASGITTYEDR-PSKAPSFWKYIDPSTHQTQGYRTVOLVWKTLPPEE 358
 QY 672 SLCSVORYVINHTSCNGWSEVGNH---TKFTFLWTEQAHTVTVLAINSIGASVANF 727
 Db 359 ANGKILDYEV-----LTRKWSHLQNTYVATKLTNLTNDRYLATLVNRLNVGKSDAAV 413
 QY 728 NTFSPMKSKNVIVQSLSAYPLNSSCVIVSWILSPSDYKLMFYIEKWNLEDGE--IKW 785
 Db 414 LTIAPACDFQATPHVMDLKAPP-KDNMLWVETTPRESVK--KYLEMVCVLSDKAPCITDW 470
 QY 786 LRISSSVKYYIYHG 799
 Db 471 QEDGTVHRTYLRG 484

```

RESULT 6
ID IL6B_RAT STANDARD; PRT; 918 AA.
AC P40190;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
GN IL6ST.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93052397; PubMed=1427893;
RA Wang Y., Nesbitt J.E., Fuentes N.L., Fuller G.M.;
RT "Molecular cloning and characterization of the rat liver IL-6 signal
RT transducing molecule, gp130.";
RL Genomics 14:666-672(1992).
CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
CC IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
CC EMBRYONIC DEVELOPMENT (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
CC AND ENDOTHELIAL CELLS.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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CC -----
DR EMBL; M92340; ; NOT_ANNOTATED_CDS.
DR PIR; A44257; A44257.
DR HSSP; P40189; 1BQU.
DR InterPro; IPR001777;
DR InterPro; IPR002465;
DR Pfam; PF00041; fn3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
DR Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
DR Repeat.
FT SIGNAL 1 22
FT CHAIN 23 918
FT DOMAIN 23 618
FT TRANSMEM 619 640
FT DOMAIN 641 918
FT DOMAIN 26 120
FT DOMAIN 124 221
FT DOMAIN 222 323
FT DOMAIN 324 422
FT DOMAIN 423 516
FT DOMAIN 517 612
FT DOMAIN 724 754
FT DISULFID 134 144
FT DISULFID 172 181
FT CARBOHYD 43 43
FT CARBOHYD 61 61
FT CARBOHYD 83 83
FT CARBOHYD 131 131
FT CARBOHYD 157 157

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FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 389 389 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 477 477 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 918 AA; 102450 MW; 9E18B6FECFF087F7 CRC64;

Query Match 6.2%; Score 270.5; DB 1; Length 918;
Best Local Similarity 22.6%; Pred. No. 5.1e-12;
Matches 116; Conservative 98; Mismatches 215; Indels 85; Gaps 25;

QY 327 VFTTQDVI-----YFPKKILTSVGSNVSFHCYIKKENKIVPSKE---IVWMNLAEL 374
DB 14 IELTTEISGLVPCGYIYPEPPVQVGRSNTATCVLKEKCLQVYSVNTYIVWTKNHV- 72
QY 375 KIPQSOYDVVSDHVSKVTFNENETKPRGFTYDAVY-----CCNEHECHHRYAEIYVI- 428
DB 73 AVPKQVTVINRTASSTVF-----TDVVFQNVQLTCNLSFGQIEQNVYGIT 119
QY 429 -----DVNINISC-ETDGYLTMTKTCRHSSTSIQSLAESTLQIYHRSSLYCSDIPSIH 480
DB 120 ILSGYPPDIPITNLSCIVNEG--KNMLCO-----LDPGRITYLETNYTLKSEWATE----- 167
QY 481 PISEPKDCYVQSDGFEYCI--FOPIFLSLSGYTMWIRINHSGLSDSPPTCVLPDSWKPL 538
DB 168 ---KFPDCTK-HGTSSCMGTYPIYFVN-IEVWVEAENALGNVSEPFNFPDVKVPS 222
QY 539 PPSSVKAETINI-GLLKISW-----EKVPFPENNLQFOIRYGLSGKEVQMKMYEYDAK 592
DB 223 PPHNLSTVNSELSILKLAWVNSGLDSTLRKSDIQVTRKDAST-----WIOVPLEDTV 277
QY 593 SKSVSLPVDL--CAVAVQVREKRLDGLGYSWNKSNPAYTVVMDIKVPMRCPETWRIIN 650
DB 278 SPRTSFTVDLKPFTFYFRINSIKENKGYWSDWSEASGTTYEDR-PSKAPSFYKVN 336
QY 651 GDTMKKEKNVTLMLKPLMKNDLSVQRY--VINHTSCNGTWSDEDVGNHTKFTFLWTEQ 708
DB 337 ANHPQEYSARLINKTLPSEANGKILDEYVVLVTQSKVSQTYTV---NGTELVNLINN 393
QY 709 AHTVTVLAINSIGASVANFNLTFSHPMSKV-NIVOSLSAYPLNNSCVIVSWILSPDYKL 767
DB 394 RYVASLAARNVGVKSPATV-LTIPGSHFKASHPVVDLKAFP-KONLLWVEW--TPPSKPV 449
QY 768 MYFIEMKNLNEDEGEI--KWLRISSSVKKYIYTHG 799
DB 450 NKYLEWCVLSENSEPCIPDWOEDGTVNRTHLRG 483

RESULT 7
ID GCSR_MOUSE STANDARD; PRT; 837 AA.
AC P40223;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GRANULOCYTE COLONY STIMULATING FACTOR RECEPTOR PRECURSOR (G-CSF-R).
DE CSF3R OR CSFGR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90235283; PubMed=2158861;
RA Fukunaga R., Ishizaka-Ikeda E., Seto Y., Nagata S.;
RT "Expression cloning of a receptor for murine granulocyte colony-
RT stimulating factor";
RL Cell 61:341-350(1990).
RN [2]
RP STRUCTURE BY NMR OF 225-333.
RX MEDLINE=97331327; PubMed=9187659;

```


Db 396 TFLPSEAEVALVAYNSAGTSRPT-PVVS--ESRGPALTELHAMDPSLWGVH--E 450

QY 762 PSDYKLYATFIIEW 774

Db 451 PPNPPOGVVIEW 463

RESULT 9

LIFR_HUMAN STANDARD; PRT: 1097 AA.

AC P42702;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE LEUKEMIA INHIBITORY FACTOR RECEPTOR PRECURSOR (LIF-R).

GN LIFR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=92007727; PubMed=1915266;

RA Gearing D.P., Thut C.J., Vandenbos T., Gimpel S.D., Delaney P.B.,

RA King J., Price V., Cosman D., Beckmann M.P.;

RT "Leukemia inhibitory factor receptor is structurally related to the

RT IL-6 signal transducer, gp130.";

RL EMBO J. 10:2839-2848(1991).

CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. MAY HAVE A COMMON PATHWAY

CC WITH GP130. THE SOLUBLE FORM INHIBITS THE BIOLOGICAL ACTIVITY OF

CC LIF BY BLOCKING ITS BINDING TO RECEPTORS ON TARGET CELLS.

CC -1- SUBUNIT: HETERODIMER COMPOSED OF LIFR AND GP130.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THERE IS A

CC MEMBRANE-BOUND AND A SECRETED FORM.

CC -1- ALTERNATIVE PRODUCTS: THE SECRETED AND THE MEMBRANE-BOUND FORMS

CC MAY ARISE BY ALTERNATIVE SPLICING.

CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

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CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL: X61615; CAA43805.1; -

DR MIM: 151443; -

DR InterPro: IPR000950; -

DR InterPro: IPR001777; -

DR Pfam: PF00041; fn3; 4.

DR PROSITE: PS01353; HEMATOPO_REC_LF2: 1.

DR Receptor: Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;

KW Alternative splicing; Repeat.

KW SIGNAL 1 44

FT CHAIN 45 1097 POTENTIAL.

FT DOMAIN 45 833 LEUKEMIA INHIBITORY FACTOR RECEPTOR.

FT TRANSMEM 834 858 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 859 1097 POTENTIAL.

FT DISULFID 55 65 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 64 64 BY SIMILARITY.

FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 243 243 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 407 407 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 426 426 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 489 489 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 572 572 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 652 652 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 663 663 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 680 680 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 729 729 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 787 787 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 1097 AA; 123742 MW; C8602897E359FCE5 CRC64;

Query Match 5.18; Score 221.5; DB 1; Length 1097;

Best Local Similarity 20.08; Pred. Nq. 2.4e-08;

Matches 143; Conservative 127; Mismatches 292; Indels 153; Gaps 33;

QY 161 LLYVLPVLEDSPLVPKQSFQMVHC-----NCS-----VHECC----- 194

Db 35 LLYLMNVNSQ-----KRGAPHLKCVTNLQVWNCWKAPSGTGRGTDYEVCIENRSRS 89

QY 195 -----ECLVPVPTAKLNDTLMLCKITSGGVIFQSPMSVQPINNVKPPDPPLGLHMEIT- 248

Db 90 CYOLEKTSIKIPALSHGDIYETINSLHDFGSSTSKFTLNQVNSLI-PDPIELNLSADF 148

QY 249 DDGNLKIWSPPPLVPPPYQYVKYSENSTVIR-----EADKIVSATSLL----- 294

Db 149 STSTLYLKWNDRGVS-PPHRSNVIW---EIKVLKESMELVKLVHTNTTLNGKDTLHWS 204

QY 295 --VDSILPGSSYEVQVR-----GKRLDGPGLWSQDSTPRVET---TQDVIYPPKILTSVG 345

Db 205 WASDMPLECAHFEIRCYIDNLHFSGLEWSQMSVKNISWIPDSOTKVFPPQDKVILVG 264

QY 346 SNVSFHCIIYKKNKIVPSKEIVVMNLAEKIPQSYQVW---SDHVSQVTFNFKETKPR 402

Db 265 SDITFCVCV-----SQEKV---LSALIGHTNCPILHLDGENVA-IKIRNISVSASS 310

QY 403 GKFTYDAYCCNHECHRYAEALYVIDVNISETGYLTKTCRWSTSTQSLA---E 459

Db 311 GT---NVVFTEDNIFGTIVFAGYPPDTPQOLNCETHD-LKEICISWNPGRVTALVGPA 366

QY 460 STLQLRVHRSLLYCSIDPSIHPISSEKDCVQLQSDGFEYCFQPIELLSGVTMTIRINSL 519

Db 367 TSYLVESFSGKYRLKRAAPTNS-----YQLLFQMLPNOEIYNTLNAHNP 416

QY 520 GSDSPPTCYLPDSVVKVPLPSPVSKAEITINIGLLKISWEKP-----VFPE 566

Db 417 GRSGSTLVNITEKVY-PHPTSFVKV-DINSTAVKLSHLPGNFAKINCELEIKSN 474

QY 567 NLOFQIRGLSGKEVQWKYEVYDAKSKSVLPVDPDLCAYVAVQVRCRDLGLGYWNS 626

Db 475 SVQEQRNVTIKGE-----NSSYLVALDKLPNTLYTTFIRCS-TETFWKNSKS 523

QY 627 NPATVVMIDIKVPMRGPEFWRIINGDTMKKEKNVTLLKPLMKNDLSQVQRYVINHTS 686

Db 524 NKQHLTTEAS-PSKGPDTWREWSSD-----GKNLIYWKLPINEA-----NGKLLSTNVS 574

QY 687 CNG-----TWSEVDGNHKTFTFLWTEQAHTVTVLAINSIGASVANFLTFSPKSNYIV 741

Db 575 CSSDEETQSLSEIPDPQHKAEIRLDKNDYIISVAKNSVGSPPSKIASMEIPNDLAKIE 634

QY 742 QSLSAVPLNSSCVISWILSPS---DYKLMYFIEWKN--LNEDGEIKWIRISS 791

Db 635 QYVGM-----GKGLLTWHYDPNMTCDY-----VIKWCNSRSEPCLDWKRKVP 680

RESULT 10

LIFR_MOUSE STANDARD; PRT: 1092 AA.

ID LIFR_MOUSE

AC P42703;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE LEUKEMIA INHIBITORY FACTOR RECEPTOR PRECURSOR (LIF-R) (D-FACTOR/LIF

FT	CARBOHYD	402	402	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	421	421	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	440	440	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	453	453	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	476	476	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	567	567	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	647	647	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	658	658	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	675	675	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	724	724	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	782	782	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	VARSPLIC	718	719	AP -> EA (IN SECRETED ISOFORM).	
FT	VARSPLIC	720	1092	MISSING (IN SECRETED ISOFORM).	
SEQ	SEQUENCE	1092 AA;	122573 MW;	6F02B8C8E154DE70	CRC64;

Query Match 4.8%; Score 208; DB 1; Length 1092;
 Best Local Similarity 19.6%; Pred. No. 2.3e-07;
 Matches 144; Conservative 125; Mismatches 271; Indels 196; Gaps:

QY	178	KGSGFMVHCNSVHECCCLVPVP	-----TAK-----LNDFTLLMC-----LKITSGGVIFQSP-	225
DB	45	KRGVQDLKCTNNRMVWDCWTWPAPGVSGTVKDIKORFHSCHPLETNNKVPALSP	104	
QY	226	-----LMSVQPINMKVPDPPLGLHMEITDD-----GNLKISWS--PPLVPF	265	
DB	105	DHEVTYINLNGFOSKFTLNEKOVSLIPETPEI-----LDLSADFTSLLLKWDGRGSA	161	
QY	266	P--LQVQVYKSENSTTVIREADKIVSATSLL-----VGSILPGSSVYVOVRGK	311	
DB	162	PSNATWEIKVQLNPR--EPVALVLLNTMLSGDKTVQHNWNTSOLPLQCATHSVSIR-	217	
QY	312	RLDGPGI-----WSDKSTPRVFT---TQDVIVPPKILTSGVSNYSFHCYKKNKIVPS	363	
DB	218	HIDSPHFSGYKESWDSPLKNIWSIRNTETNVFPQDKVVLGASNMTICC-----MSPT	270	
QY	364	KEIVWM--NLAEKIPOSQDVVSDHVSKVTFNMLNETKPRGK-----FTYDAVVCNEHEC	418	
DB	271	KVLSGOIGNTLRPLIHLGYOTVAIH-----LNIPVSENSGNIILFITDDV-----	317	
QY	419	HRYAEL-----YVIDVNISETDGYLTKMTCRWSTTQSL-----AESTL-----	462	
DB	318	---YGTVVFAGYPPDVQPLSCETHD-LKEIICSWNPGRITGLVGPRTYETLFEISIGK	373	
QY	463	QLRYHR-----SSLXCSDIPTSHPISEPKCYLQSDGFYECIFQPIFLLSGYTMIRINH	517	
DB	374	SAVFHRIEGLTETRYBLGV-QMHPQGEIHN-----FTLTG-----RN	409	
QY	518	SLGSDSPPTCVLPDSVWRPLPSPSSVKABEITINIGLLKISWEKP--VFPENNLFQIRYGL	576	
DB	410	PLGQAQSAVVINVTERVA--PHDPTSLVKV--DINSTVVTFSWLPNGFTKINLLCQIECK	467	
QY	577	SKQEVQWKMYEYVDAKSVSLVPDPL--CAVYAVQVRCRKLGLGYWNSNPNAYTVVM	634	
DB	468	ANSKKEVRNATIRGAEDSTYHVAVDKLNPYATYATERVRCSS-KTFWKWSRWSDEKRLHT	526	
QY	635	DIKVPMRGPEFWRIINGDPMPKKEKNVTLWLKPLMKNDLSLCVQRYVINHTSCNGTWS	694	
DB	527	E-ATPSKGDDTREWSSD-----GKNLIVYMKKPLPINEA-----NGKLISYNVSS	571	
QY	695	VGNHTKFTLWTEQAH-----TVTVLAINSIGASVANENLTSWPMKSVKNIVQS	743	
DB	572	LNREETQSULEIFDPQHRABIQISKNDYIISVVARNSAGSSPPSKTASMEIPNDITVEQA	631	
QY	744	LSAYPLUNSCVIVSWILSPS-----DYKLMYFIIEWKN--LNEDEGIKWLRISSVKK	794	
DB	632	VGL---GNRIELTWHDNMTCDY-----VIKWCNSSRSEPCLLDWRKVPSPNSTETVIE	682	
QY	795	-----YYIHG	799	
DB	683	SDQFQPGVRYNFYLG	698	

```

RESULT 11
ID 1125_MOUSE STANDARD; PRT; 874 AA.
AC P37378;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN PRECURSOR (IL-12 RECEPTOR BETA-2) (IL-12R-BETA2).
DE 2) (IL-12R-BETA2).
GN IL12RB2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97098510; PubMed=8943050;
RA Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y.,
RA Gately M.K., Gubler U.;
RT *A functional interleukin 12 receptor complex is composed of two
RT beta-type cytokine receptor subunits.*;
RL Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).
CC -1- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A
CC LOW AFFINITY.
CC -1- SUBUNIT: DISULFIDE-LINKED HOMODIMER/OLIGOMER. THE FUNCTIONAL HIGH
CC AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND
CC IL12RB2.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U64199; AAB36676.1; -
CC HSP; P40189; 1BQ.
CC MGD; MGI:1270861; IL12RB2.
CC InterPro; IPR001777; -
CC InterPro; IPR002465; -
CC InterPro; IPR002996; -
CC Pfam; PF00041; fn3. 4.
CC PROSITE; PS0014; FNTYPEIII.
CC PROSITE; PS01353; HENATOPO_REC_L_F2; 1.
CC Receptor; Transmembrane; Glycoprotein; Signal; Repeats
CC SIGNAL 1 20
CC CHAIN 21 874
CC DOMAIN 21 639
CC TRANSMEM 640 656
CC DOMAIN 657 874
CC DOMAIN 137 230
CC DOMAIN 240 322
CC DOMAIN 436 523
CC DOMAIN 534 622
CC CARBOHYD 48 48
CC CARBOHYD 101 101
CC CARBOHYD 114 114
CC CARBOHYD 142 142
CC CARBOHYD 151 151
CC CARBOHYD 169 169
CC CARBOHYD 179 179
CC CARBOHYD 224 224
CC CARBOHYD 252 252
CC CARBOHYD 279 279
CC CARBOHYD 287 287
CC CARBOHYD 323 323
CC CARBOHYD 391 391
CC CARBOHYD 495 495
CC SEQUENCE 874 AA; 98196 MW; 58284D21BF1FD67 CRC64;

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Query Match 4.7%; Score 205.5; DB 1; Length 874;
Best Local Similarity 24.9%; Pred. No. 2.6e-07;
Matches 104; Conservative 51; Mismatches 156; Indels 107; Gaps 25;

QY 433 NISCETGYTKMTCRWSTSTIOSLAES-TIQRYHRSSLYCSDIPSIHPISEPKCYLQ 491
    |||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 142 NISCVOGEGTGVACSWNSGKVTYTKNTYLTQLS-GPNLTQC-----KQCF-- 187

QY 492 SDGFYEC-----IFQIFLLSGYTMIRINSLSDSPPTCVLPDSVVKPLPPSSVK 544
    || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 188 SDNRQNCNRDLGILNLSPLDAESRFIVRTAINDLGNSSSLPHTFTFLDVIPLPPMDIR 247

QY 545 AEITINIGLKIS-----WE-KPVEPENNIQFIIRYGLSGREVQMKYEVDAKSKSV 596
    - - - - - INFLNAGSGRGTLQWDEGGVVLNQLRYQPLNSTS-----WNMYNATNAKGG-- 294
Db 248 -----INFLNAGSGRGTLQWDEGGVVLNQLRYQPLNSTS-----WNMYNATNAKGG-- 294

QY 597 SLVPDL--CAVYAVQVRCK-RLDGLGYWNSNPAYTVVMDIKVPMRGP-----EFWRII 649
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 295 -YDLRLDLPFTYEFQISSKHLHSG-GSWNSWSESLRT-----RTPEEPVGILDIW-YM 346

QY 650 NGDTMKKEKNVTLWKPLMKNDSLCSVQRYVINHTSCNCTWSEDVGNHTKFTFLATE-- 707
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 347 QKDDIDYDQOISLFWKSLNPSEARGKILHYQVTLQEVTKTKTLQNTTRHTS-----WTRVI 402

QY 708 ---QAHTVTVLAINSIGASVANFNLTFSWPMKSNIV-----QSLSAAYPLNSSCV 754
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 403 PRGTAWTASVSAANSKASAP-----THINIVDLGCTGLLAPHQVSAKSENMDNI 452

QY 755 IVSWILSP---SDYKLMFYFIKWNLMNEDGEI-----KWLR-----ISSVKKY 795
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 453 LVTV--QPPKKASAVREYIVEWRAL-QPSITKFPHPHLRIPPDMNSALISNIKPY 507

RESULT 12
ID 1125_HUMAN STANDARD; PRT; 862 AA.
AC Q99665;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN PRECURSOR (IL-12 RECEPTOR BETA-2) (IL-12R-BETA2).
DE 2) (IL-12R-BETA2).
GN IL12RB2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97098510; PubMed=8943050;
RA Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y.,
RA Gately M.K., Gubler U.;
RT *A functional interleukin 12 receptor complex is composed of two
RT beta-type cytokine receptor subunits.*;
RL Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).
CC -1- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A
CC LOW AFFINITY.
CC -1- SUBUNIT: DISULFIDE-LINKED DIMER/OLIGOMER. THE FUNCTIONAL HIGH
CC AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND
CC IL12RB2.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC EMBL; U64198; AAB36675.1;
DR HSP; P40189; 1BQ.
DR MIN; 601642;
DR InterPro; IPR001777;
DR InterPro; IPR002465;
DR InterPro; IPR002996;
DR Pfam; PF00041; fn3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 21
FT CHAIN 22 862
FT DOMAIN 22 624
FT TRANSMEM 625 641
FT DOMAIN 642 862
FT DOMAIN 224 306
FT DOMAIN 421 508
FT DOMAIN 519 607
FT CARBOHYD 48 48
FT CARBOHYD 129 129
FT CARBOHYD 166 166
FT CARBOHYD 195 195
FT CARBOHYD 271 271
FT CARBOHYD 347 347
FT CARBOHYD 376 376
FT CARBOHYD 480 480
SQ SEQUENCE 862 AA; 971134 MW; 67C0E0D946B8DD58 CRC64;

Query Match
Best Local Similarity 4.6%; Score 200.5; DB 1; Length 862;
Matches 115; Conservative 79; Mismatches 208; Indels 121; Gaps 27;

QY 332 DIVYFPKILTSVGSNVSPHCI-----YKKNKIVPSKEIVWMNLAEKIPQSOYD 382
DB 32 DVTVKPSHVL-LGSVNTICSLKPGQCFHYSRKNLLIYK-----FD 74

QY 383 -VVSDH-----VSKVTFNLTNPKRGKTYDAVYCCNHECHRYAEIYV--IDVNI 433
DB 75 RRIHFHGHSLNSOVTGLPTGLTFLVCKLA-----CINSDEIQICGAEIFVGVAPEQPON 129

QY 434 ISCETDGLTKMTCTWSTSTIQSL-AESTLQRLYHRSSLY---CSDIPSIHPISEPKDC- 488
DB 130 LSCIQKGEGTACTWGERDTHLTETYLQSLGPKNLTWQKQCKDI-----YCD 179

QY 489 YLQSDGFYECIFQIFLLSGYTWIRINHSGLSDSPCTCVLPDSVWKPPLPSSVKAET- 547
DB 180 YLD-----FGINLTSPESPENFTAKVTAVNSLSSSLSTFTFLDIVRPLPWRIRIKFQ 235

QY 548 TINIGLLKISWEKVPFPENNLOFQIRYGLSGKEVQWKMVEYVDAKSQSVLPVPDLCAVY 607
DB 236 KASVSRCITLYMRDEGLVLLN---RLRYPNSRL-WNNVNTKAKGRHDLDLKPF-TEY 290

QY 608 AVQVRCKRLDGLGYSNKSNAPYVVMIDIKVPMRGP-----EPWRIINGDTAKK-----EK 658
DB 291 EQIISKHLHYKGSNDSES-----LRAQTPDEEPTGMLDVW-----YMKRHIDYSRQ 339

QY 659 NYTLWPKLPMKNLSCSVQRYVINHTSCNG-TWSEYVGNHTKFTFLWTEQAH-TVTVLA 716
DB 340 QISLFWKLNLSVEARGKILHYQVTLQELTGKAMQNTGHTSWTVIPRTGNVAVAYSA 399

QY 717 INSIGASVANFLTSPWPKVNIY-----QSLGAYPLNSCCVIVSWILSPSD-Y 765
DB 400 ANSKGSSLP-----TRINIMLCEAGLLAPROVANSANSEGMNLTWQPRKDPDS 449

QY 766 KMYPIIEMKLNLEDGE-----IKWLR-----ISSVVKY 795
DB 450 AVQEVVWEVREHLPGDQVPLNLRSPRYNVSALISENIKSY 492

```

RESULT 13

PRLR_MELGA

ID PRLR_MELGA

STANDARD;

PRT; 831 AA.

```

AC Q91094; Q91091; Q91092;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (TPRLR).
OS PRLR.
GN Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagridae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
TX TISSUE-Kidney;
RX MEDLINE=97057891; PubMed=8902221;
RA Zhou J.F., Zadowny D., Guemene D., Kuhnlein U.;
RT "Molecular cloning, tissue distribution, and expression of the
RT prolactin receptor during various reproductive states in Meleagris
RT gallopavo.";
RL Biol. Reprod. 55:1081-1090(1996).
RN [2]
RP SEQUENCE OF 82-121 AND 473-522 FROM N.A.
TX TISSUE-Ovary;
RA Pitts G.R., You S.K., Foster D.N., el Halawani M.E.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC
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CC
EMBL; L76587; AAB01544.1;
DR EMBL; U22947; AAB75038.1;
DR EMBL; U22924; AAB75039.1;
DR HSP; P16471; 1BP3.
DR InterPro; IPR000950;
DR InterPro; IPR001777;
DR InterPro; IPR002465;
DR Pfam; PF00041; fn3; 4.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 831
FT DOMAIN 24 438
FT TRANSMEM 439 459
FT DOMAIN 460 831
FT DOMAIN 25 122
FT DOMAIN 123 225
FT DOMAIN 228 325
FT DOMAIN 326 428
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 262 262
FT CARBOHYD 303 303
FT CARBOHYD 315 315
FT CARBOHYD 335 335
SQ SEQUENCE 831 AA; 94394 MW; 220916320F77FAC1 CRC64;

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Query Match

Best Local Similarity

4.1%; Score 181; DB 1; Length 831;

20.4%; Pred. No. 1.5e-05;

Matches 92; Conservative 58; Mismatches 123; Indels 178; Gaps 21;

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QY 229 VQINMVKPDPPLGLHMEITDDGNLKISWS--SPPLVP-----FPLQYQVKYSENS 277
Db 119 VDVTSIVQPGSPVNLTLTORYANIMYLAKWSPPLLADASSNNHLYHYELRKPEKEEW 178
QY 278 TTVTREADKIVSATSLLVDSILPGSSVEQVRKRLDGPGLGWSDMSTPRVFTQDVIYFP 337
Db 179 ETV-----PVGVOQCKINRLNAGMRYVQVR-CMLD-PGEWSEWSSER-----220
QY 338 PKILTSVGSNVSFHCIIYKKNKIV-----PSKE--IYWMNLAEKIPQSYQVVDVSHVSK 390
Db 221 -RLISGG-----LSPPEKPIITKRSPEKETFTCW-----251
QY 391 VTFPNLAETKRGFTYDVAVYCCNEHECHRYAELVYIDVININISCTDGYLTKMTCRWS 450
Db 252 -----KPG-----LD-----GGHPTNYTLTYS 268
QY 451 TSTIQSLAESTLQLYHRSSLYCSDIPSIHPISEPKCYL--QSDGYECIFQIFLLSG 508
Db 269 KEGEQYVE-----CPD-----YRTAGPNSCYFDKHTSFW-----TV 301
QY 509 YTMIRINHSILGSLDSPPTCVLPDSVVKPLPPSSVKAEL-----T 548
Db 302 YNTVKATNMGSSNDSPHYDVIYVQPPANVTLELKKPINRKPYLMLTWSPPPLAD 361
QY 549 INTGLLAKISWEKVPFENNIFQIRYGLSGKEVQWKMVEYDAKSKSVSLPVDLCAYYA 608
Db 362 VRSGLTLDYELRLKPEGEWETVF--VGQOYQKMFSLNPGKK-----YI 406
QY 609 VQVRCRLDGLGYWSNWSNPAYTVVMDIKVP 639
Db 407 VQIHCKP-DHHSWSEWSSENY-----IEIP 431

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RESULT 14

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PRLR_CHICK STANDARD; PRT; 831 AA.
AC Q04594;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (CPLRP).
GN PRLR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LECHORN; TISSUE-Kidney;
RX MEDLINE=93075121; PubMed=1445292;
RA Tanaka M., Maeda K., Okubo T., Nakashima K.;
RT Double antenna structure of chicken prolactin receptor deduced from
RL the cDNA sequence.*;
RC Biochem. Biophys. Res. Commun. 188:490-496(1992).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D13154; BAA02439.1;
DR PIR; JQ1655; JQ1655.

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DR HSSP; P16471; 1BP3.
DR InterPro; IPR000950;
DR InterPro; IPR001777;
DR InterPro; IPR002465;
DR Pfam; PF00041; fn3; 4.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
FT SIGNAL 1 23
FT CHAIN 24 831
FT DOMAIN 24 438
FT TRANSMEM 439 459
FT DOMAIN 460 831
FT CYTOPLASMIC (POTENTIAL).
FT FIBRONECTIN TYPE-III.
FT DOMAIN 123 225
FT FIBRONECTIN TYPE-III.
FT DOMAIN 228 325
FT FIBRONECTIN TYPE-III.
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 91
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 262 262
FT CARBOHYD 303 303
FT CARBOHYD 315 315
FT CARBOHYD 335 335
FT CARBOHYD 335 335
SQ SEQUENCE 831 AA; 94102 MW; 1C4E75791DCADB9 CRC64;

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Query Match 4.1%; Score 178; DB 1; Length 831;

Best Local Similarity 20.4%; Pred. No. 2.5e-05;

Matches 91; Conservative 55; Mismatches 133; Indels 166; Gaps 21;

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QY 229 VQINMVKPDPPLGLHMEITDDGNLKISWS--SPPLVP-----FPLQYQVKYSENSTT 279
Db 119 VDVTSIVQPGSPVNLTLTQRSANIMYLAKWSPPLLADASSNNHLYHYELRKPEKEEW 178
QY 280 VIREADKIVSATSLLVDSILPGSSVEQVRKRLDGPGLGWSDMSTPR--VFTQDVIYF 336
Db 179 ---ETISVGVOQCKINRLNAGMRYVQVR-CYLD-PGEWSEWSSERHILPSCQS-----229
QY 337 PKILTSVGSNVSFHCIIYKKNKIVPSKE--IYWMNLAEKIPQSYQVVDVSHVSKVTF 394
Db 230 PPEKPTIKR-----SPEKETFTCW-----251
QY 395 NLNETPRGRFTYDVAVYCCNEHECHRYAELVYIDVININISCTDGYLTKMTCRWSTSI 454
Db 252 -----KPG-----LD-----GGHPTNYTLTYSKEGE 272
QY 455 QSLAESTLQLYHRSSLYCSDIPSIHPISEPKCYLQSDGYECIFQIFLLSGYTMWIR 514
Db 273 EQYVE-----CPD-----YRTAGPNSCYFDKK---HTSFWTI-----YNTVR 307
QY 515 INHSLGSLDSPPTCVLPDSVVKPLPPSSVKAEL-----TINIGLL 554
Db 308 ATNEMGSNDSPPHYDVIYVQPPANVTLELKKPINRKPYLVLTVSPPLADVRSGLW 367
QY 555 KISWEKVPFENNIFQIRYGLSGKEVQWKMVEYDAKSKSVSLPVDLCANTAVQVRCK 614
Db 368 TLEYELRLKPEGEWETIF--VGQOYQKMFSLNPGKK-----YIIHQCK 412
QY 615 RLQGLGYWSNWSNPAYTVVMDIKVP 639
Db 413 P-DHHSWSEWSSENY-----IQIP 431

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RESULT 15

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LAR_DROME STANDARD; PRT; 2029 AA.
ID LAR_DROME
AC P16621;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)

```

DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (EC 3.1.3.48) (PROTEIN-
GN TYROSINE-PHOSPHATE PHOSPHOHYDROLASE).
OS Lar.
OC Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90046860; PubMed=2554325;
RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;
Rt "A family of receptor-linked protein tyrosine phosphatases in humans
and Drosophila.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON-S;
RX MEDLINE=96178473; PubMed=8598047;
RA Krueger N.X., van Vector D., Wan H.I., Gelbart W.M., Goodman C.S.,
Rt "The transmembrane tyrosine phosphatase DLAR controls motor axon
guidance in Drosophila.";
RL Cell 84:611-622(1996).
CC -1- FUNCTION: IT IS POSSIBLE THAT DLAR IS A CELL ADHESION RECEPTOR.
CC IT POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY
CC (PTPASE). IT CONTROLS MOTOR AXON GUIDANCE.
CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =
CC PROTEIN TYROSINE + ORTHOPHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: SELECTIVELY EXPRESSED IN A SUBSET OF AXONS AND
CC PIONEER NEURONS IN THE EMBRYO.
CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 16 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
CC -----
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CC -----
DR EMBL; M27700; AAC28668.1; -;
DR EMBL; U36857; AAC47002.1; -;
DR EMBL; U36849; AAC47002.1; JOINED.
DR EMBL; U36850; AAC47002.1; JOINED.
DR EMBL; U36851; AAC47002.1; JOINED.
DR EMBL; U36852; AAC47002.1; JOINED.
DR EMBL; U36853; AAC47002.1; JOINED.
DR EMBL; U36854; AAC47002.1; JOINED.
DR EMBL; U36855; AAC47002.1; JOINED.
DR EMBL; U36856; AAC47002.1; JOINED.
DR PIR; A36182; TDFELK.
DR HSP; P28827; IRPW.
DR Flybase; FBgn0000464; Lar.
DR InterPro; IPR000242; -;
DR InterPro; IPR000387; -;
DR InterPro; IPR001777; -;
DR InterPro; IPR003006; -;
DR Pfam; PF00102; I-phosphatase; 2.
DR Pfam; PF00041; fn3; 9.
DR Pfam; PF00047; fn3; 9.
DR PRINTS; PR00014; FNTYPEIII.
DR PRINTS; PR00700; PTPYRPHPTASE.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS00386; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS00556; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS00555; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
KW Cell adhesion; Immunoglobulin domain; Duplication.
FT SIGNAL 1 32

CHAIN	33	2029	PROTEIN-TYROSINE PHOSPHATASE DLAR.
FT DOMAIN	33	1377	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	1378	1402	POTENTIAL.
FT DOMAIN	1403	2029	CYTOPLASMIC (POTENTIAL).
FT DOMAIN	50	118	IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN	154	216	IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN	249	308	IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN	320	417	FIBRONECTIN TYPE-III 1.
FT DOMAIN	418	512	FIBRONECTIN TYPE-III 2.
FT DOMAIN	513	607	FIBRONECTIN TYPE-III 3.
FT DOMAIN	608	706	FIBRONECTIN TYPE-III 4.
FT DOMAIN	707	809	FIBRONECTIN TYPE-III 5.
FT DOMAIN	810	906	FIBRONECTIN TYPE-III 6.
FT DOMAIN	907	1007	FIBRONECTIN TYPE-III 7.
FT DOMAIN	1008	1102	FIBRONECTIN TYPE-III 8.
FT DOMAIN	1103	1207	FIBRONECTIN TYPE-III 9.
FT DOMAIN	1492	1738	PROTEIN-TYROSINE PHOSPHATASE.
FT DOMAIN	1781	2029	PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE	1670	1670	BY SIMILARITY.
FT ACT_SITE	1961	1961	BY SIMILARITY.
FT DISULFID	57	111	POTENTIAL.
FT DISULFID	161	209	POTENTIAL.
FT DISULFID	256	301	POTENTIAL.
FT CARBOHYD	176	176	N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	253	253	N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	298	298	N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	553	553	N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	616	616	N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	666	666	N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	721	721	N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	774	774	N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	915	915	N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	962	962	N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	1183	1183	N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	1304	1304	N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD	2029	2029	N-LINKED (GLCNAC. .) (POTENTIAL).
FT SEQUENCE	2029	22907	MM; 536A0C794D3DC800 CRC64;
SEQ			

Query Match 3.8%; Score 166.5; DB 1; Length 2029;
Best Local Similarity 18.7%; Pred. No. 0.00056;
Matches 123; Conservative 119; Mismatches 257; Indels 159; Gaps 32;

QY 218 GGVIFQSPMLSVQPINMKVPDPPL-----GLHMEITDGNLKIWSPPPLVPFPLQYQ- 270
DB 90 GGI-----SILRIEPRAGRDADPYECVAENGVDASADATLTIEGDKTPAGFPVITQG 145
QY 271 --VKYSENSTVIREADKIVSATSL-----VDSILPGSSYE---VQVRGRKLDGPG 317
DB 146 PGRVIEVGHVTLMTCKAIGNPTNIIWKTKVDMSNPRYSKLDGFLQIENSREEDQG 205
QY 318 IW-----SDWSTPRVFTTQDVIYF-----PPKILTSV--GSNVSFHCIVKKENK 359
DB 206 KYECVAENSMGTESKATN--LYVKVRVRVPPTFSRPETISEVMLGSLNLSIAVGS-- 261
QY 360 IVPSEIYVWMNLAEKIPQSQVDVVDVSKVTFNLMETKPRKFTYDQVYCCNEHECH 419
DB 262 --PMHVKVMKGSDELTPENEMPIGRNVQLI---NIQES-----ANYTCAASTL 307
QY 420 HRYAELYYIDVYNINISCTDGYLTMTKC-----RNSTSTIQSLAESTQLRHYRSLVCS 474
DB 308 GOIDSVSVMKVSQSLPTAPTDQISEVTATSVLEYSKGPEDLQYVVIQYKPKNAQAFS 367
QY 475 DIPSIHPISEPKDCVQLQSDGFYECIFQPIFLLSGYTMW----IRINH--SLGSLDSPPTCV 529
DB 368 EISGI-----ITMYVVRALSPTEFEYFVIANNIGRGPSPAPACT 410
QY 530 LPDSVVKLPSPSSKAEITINIGLKIWEKVPFPENNLO--FOIRYGLSGK--EYQWKY 586
DB 411 TGETKNES--APRNQVR--TLSSSTWITWEPEPTNGQVTKYKVVYTTNSNOPEASWSQ 468
QY 587 EYDAKSKSVSLPVDLCVAVQVRCRLDGLGKWSNWSNPATYVMDIK-----VPMRG 642
DB 469 MVDNSELTVSDVTPH--AIYTVRVQ-----AYTSMGAGPMSTPV--QVRAQCGQVSPQ 518

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QY 643 PEKRIINGDTMKKEKNVTLLW-KPLMKNDLCSVQRYVINHHHTSCNGTWSDEVGNHTKF 701
Db 519 SNFRATDIGETA-----VTLQWTKPTHSSSENIHVHLY-----WNDTYANQAAH 562
QY 702 TELWTEQAHVTVLAINSIGASVANFNLTFSW-----PMSKVNIV----- 741
Db 563 KRISNSEAYTLGLYPT-----LYIWLAAARSQGEAGATPPIPVRTKOYVPGAP 613
QY 742 -QSL SAYPLNSCIVVSWILSP---SDYKLMY---FIEMKNLNEGEIKWLRISSV 792
Db 614 PRNITATSTTISLSWLPVPPVRSNGRIIYKVFVEVGREDDERATTTLANWTSIV 671

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Search completed: October 22, 2001, 16:07:46
 Job time: 190 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 22, 2001, 16:03:50 ; Search time 24.21 Seconds
(without alignments)
2013.287 Million cell updates/sec

Title: US-09-116-676-10

Perfect score: 4363

Sequence: 1 MICQKFCVLLHWEFIYIT.....WLRISVVKKYIHGKFTIL 804

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 6062398 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_0601.*

- 1: /SIDSB/gcgdata/geneseq/geneseq/AA1980.DAT.*
- 2: /SIDSB/gcgdata/geneseq/geneseq/AA1981.DAT.*
- 3: /SIDSB/gcgdata/geneseq/geneseq/AA1982.DAT.*
- 4: /SIDSB/gcgdata/geneseq/geneseq/AA1983.DAT.*
- 5: /SIDSB/gcgdata/geneseq/geneseq/AA1984.DAT.*
- 6: /SIDSB/gcgdata/geneseq/geneseq/AA1985.DAT.*
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- 8: /SIDSB/gcgdata/geneseq/geneseq/AA1987.DAT.*
- 9: /SIDSB/gcgdata/geneseq/geneseq/AA1988.DAT.*
- 10: /SIDSB/gcgdata/geneseq/geneseq/AA1989.DAT.*
- 11: /SIDSB/gcgdata/geneseq/geneseq/AA1990.DAT.*
- 12: /SIDSB/gcgdata/geneseq/geneseq/AA1991.DAT.*
- 13: /SIDSB/gcgdata/geneseq/geneseq/AA1992.DAT.*
- 14: /SIDSB/gcgdata/geneseq/geneseq/AA1993.DAT.*
- 15: /SIDSB/gcgdata/geneseq/geneseq/AA1994.DAT.*
- 16: /SIDSB/gcgdata/geneseq/geneseq/AA1995.DAT.*
- 17: /SIDSB/gcgdata/geneseq/geneseq/AA1996.DAT.*
- 18: /SIDSB/gcgdata/geneseq/geneseq/AA1997.DAT.*
- 19: /SIDSB/gcgdata/geneseq/geneseq/AA1998.DAT.*
- 20: /SIDSB/gcgdata/geneseq/geneseq/AA1999.DAT.*
- 21: /SIDSB/gcgdata/geneseq/geneseq/AA2000.DAT.*
- 22: /SIDSB/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4363	100.0	804	AAW34501	Obesity receptor p
2	4337	99.4	839	AAW34502	Obesity receptor p
3	4337	99.4	896	AAW24052	Human WSX receptor
4	4337	99.4	923	AAW24053	Human WSX receptor
5	4337	99.4	970	AAW34499	Obesity receptor C
6	4337	99.4	972	AAW34497	Obesity receptor A
7	4337	99.4	999	AAW34498	Obesity receptor B
8	4337	99.4	1165	AAW24051	Human WSX receptor
9	4337	99.4	1165	AAW113474	Peptide Seq ID No:
10	4337	99.4	1220	AAW34500	Obesity receptor D
11	4325	99.1	896	AAW50003	Human OB-R variant

12	4325	99.1	904	18	AAW50002	Human OB-R variant
13	4325	99.1	958	18	AAW38214	Human OB-R variant
14	4325	99.1	958	18	AAW31911	Human OB-R lepton
15	4325	99.1	958	18	AAW19535	Human OB-R lepton
16	4325	99.1	958	18	AAW22773	Human haematopoiet
17	4323	99.1	1165	18	AAW19116	Human OB receptor.
18	4322	99.1	898	17	AAW88912	Haematopoietin rec
19	4322	99.1	908	17	AAW88911	Haematopoietin rec
20	4322	99.1	960	17	AAW88910	Haematopoietin rec
21	4315	98.9	908	18	AAW19536	Variant form of hu
22	4296	98.5	896	18	AAW14841	Human haematopoietin
23	4234	96.6	815	20	AAW05701	Human OB receptor
24	3900	89.4	1221	19	AAW62544	Human OB-receptor
25	3355	76.9	805	18	AAW22106	Murine leptin rece
26	3345	76.7	894	18	AAW24064	Murine WSX recepto
27	3345	76.7	894	18	AAW19114	Murine short form
28	3345	76.7	900	18	AAW22105	Murine leptin rece
29	3345	76.7	1162	18	AAW19115	Murine long form O
30	3342	76.6	1162	20	AAW13473	Peptide Seq ID No:
31	3342	76.6	892	18	AAW34260	Rat ob receptor is
32	3342	76.6	894	18	AAW37337	Ob protein recepto
33	3342	76.6	895	18	AAW34258	Rat ob receptor is
34	3342	76.6	1162	18	AAW34257	Rat wild-type ob r
35	3342	76.6	1162	18	AAW33398	Rat ob receptor (w
36	3336	76.5	894	18	AAW37338	Ob protein recepto
37	3336	76.5	1162	18	AAW23399	Rat ob receptor (f
38	3143	72.0	783	18	AAW24054	Murine WSX recepto
39	3039	69.7	842	18	AAW22102	Murine leptin rece
40	2772	63.5	1015	18	AAW34259	Rat ob receptor is
41	2665	61.1	883	19	AAW62543	Human ob-receptor
42	1151	26.4	235	19	AAW62545	Soluble leptin bin
43	570	13.1	581	18	AAW22103	Murine leptin rece
44	564	12.9	319	18	AAW22104	Murine leptin rece
45	351	8.0	1158	21	AAW92205	Fusion polypeptide

ALIGNMENTS

RESULT 1

AAW34501
ID AAW34501 standard; protein; 804 AA.

XX AAW34501;

XX 18-MAR-1998 (first entry)

XX Obesity receptor protein splice variant.

XX Obesity receptor; human; OB receptor; OB receptor/OB protein complex;
XX high blood lipid level; obesity; diabetes; high cholesterol level;
XX weight loss; therapy; weight maintenance; splice variant.

XX Homo sapiens.

OS W09725424-Al.

PN 17-JUL-1997.

XX 02-JAN-1997; 97WO-US00128.

XX 31-DEC-1996; 96US-0774414.

PR 04-JAN-1996; 96US-0582825.

PA (AMGE-) AMGEN INC.

XX Chang M, Fletcher FA, Welcher AA;

PI WPI; 1997-384981/35.

DR N-PSDB; AAT98534.

XX Obesity protein receptor(s) and related DNA - used to treat weight

PT disorders, e.g. obesity, diabetes and high cholesterol or blood

Lipid levels

Claim 4; Page 89; 151pp; English.

This sequence represents a natural splice variant of the obesity (OB) receptor protein. This sequence has one or more of the biological properties of naturally occurring OB receptor protein. The OB receptor proteins and OB receptor/OB protein complexes are used for the treatment of obesity, diabetes, high blood lipid levels and high cholesterol levels. The proteins may also be used to treat an individual for weight loss or weight maintenance required for purely cosmetic purposes.

Sequence 804 AA;

Query Match 100.0%; Score 4363; DB 18; Length 804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICOKFCVLLHWEFIYVITAFNLSPYITPWRFKLSMPPNSTYDFLLPAGLSKNTS 60
DB 1 micokfcvllhwefiyvitafnlspytprwfrklscmpnstydfllpaglskntsn 60
QY 61 NGHYETAPEKFNSSGTHFNSLKTTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
DB 61 ngyetavepkfnssgthfnslnkttfhccfrseodrnscldadniegkftvstvnslvf 120
QY 121 QOIDANNIQCWLKGLDKLFCYVESLFRNLYNYKVHLLYVLPVLEDSPLVPQKGS 180
DB 121 qqidanwniqcwkglklfcyveslfrnlynykvhllylvpvledsplvpqkgs 180
QY 181 FQMVHCNCSVHECCCECLVPVPTAKLNDTLMLCKITSGGVIQSPPLMSVQPINNVKPDPP 240
DB 181 fgmvhcnscvheccceclvpvptaklndtlmlckitsggviqspplmsvqpinmvkpdpp 240
QY 241 LGHMEITDGNLKIWSPPPLVPFPQYQVYSENSTVIREADKIVSATSLLVDSIIP 300
DB 241 lghmeitdgnlkiwsppplvpfpqyqvysesttvireadkivsatsllvdsiip 300
QY 301 GSSYEVQVRGKRLDGGPGINSWSTPRVFTQDVIYPPPKILTSVGSNVSFHCYKKNKI 360
DB 301 gssyevqvrgrldgpginswstprvftqdvlyfppkiltsvgsnvsfchcykknki 360
QY 361 VPSKEIWMNNAELKIPQSDYDVSQVSHVSKVTFENLNEFKPKGTIDYAVYCCNEHECHH 420
DB 361 vpskelvwmnnaelkippqsdvsvshvskvtfenlnetkpkgtidyavycnehechh 420
QY 421 RYAEIYVIDVNIINISCTDGYLTKMTCRMTSTIQSLAESTLQRLYHRSSLYCSDIPSTH 480
DB 421 ryaeliyvidvniiniscetdgyltkmtcrwtstiqslaestlqrlryhrsglycsdipsth 480
QY 481 PISEPKDCYLOSDGFEYECIFQDIFLLSGYTMWIRNHSLSLSDSPPTCVLPDSVVKPLPP 540
DB 481 pisepkdcylodsgfeyecifqdfllsgytmwirnhsllsldspptcvlpdsvvkplpp 540
QY 541 SSVKAEITINIGLLKISWEKVPFENNIFQFIRYGLSGKEVQWKKYEVYDAKSKSVSLPV 600
DB 541 ssvkaeitinigllkiswekvpfennifqfiryglsgkevqwkkyevydaksksvslpv 600
QY 601 PDLCAVAVQVRCKRLDGLGYWSNMSNPAYTVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
DB 601 pdlcavavqvrckrldglgywsnmsnpaytvmdikvpmrgpewrilingdtmkkeknv 660
QY 661 TLLWPLMKNDLSQVQRYVINHHSTSCNGTWSVDGNHKTFTLWTEQAHRVTVLAINSI 720
DB 661 tllwplmkndlsqvqryvinhstscngtwsdvgnhktftlwteqahrvtvlainsi 720
QY 721 GASVANENLTESWPKSKVNIQVLSAYPLNSCVIVSWILSPSOYKLMFYIENKLNED 780
DB 721 gasvanenltswpkskvniqvlsayplnscvsvilspsoyklmfyienklned 780
QY 781 GEIKWLRISSSVKYYIHGKFTIL 804
DB 781 geikwlriSSSVKYYIHGKFTIL 804

Db 781 geikwlriSSSVKYYIHGKFTIL 804

RESULT 2

AAW34502
ID AAW34502 standard; protein; 839 AA.

XX AC AAW34502;

XX DT 18-MAR-1998 (first entry)

XX DE Obesity receptor protein.

XX KW Obesity receptor; human; OB receptor; OB receptor/OB protein complex;
XX KW high blood lipid level; obesity; diabetes; high cholesterol level;
XX KW weight loss; therapy; weight maintenance.

XX OS Homo sapiens.

XX PN W09725424-A1.

XX PD 17-JUL-1997.

XX PF 02-JAN-1997; 97WO-US00128.

XX PR 31-DEC-1996; 96US-0774414.

XX PR 04-JAN-1996; 96US-0582825.

XX PA (AMGE-) AMGEN INC.

XX PI Chang M, Fletcher FA, Welcher AA;

XX DR WPI; 1997-384981/35.

XX DR N-PSDB; AAT98532.

XX PT Obesity protein receptor(s) and related DNA - used to treat weight
XX PT disorders, e.g. obesity, diabetes and high cholesterol or blood
XX PT lipid levels

XX PS Disclosure; Page 82; 151pp; English.

XX CC This sequence represents the obesity (OB) receptor protein. This
XX CC sequence was used to identify the variants shown in AAW34497-W34501. The
XX CC variants have one or more of the biological properties of naturally
XX CC occurring OB receptor protein. The OB receptor proteins and OB
XX CC receptor/OB protein complexes are used for the treatment of obesity,
XX CC diabetes, high blood lipid levels and high cholesterol levels. The
XX CC proteins may also be used to treat an individual for weight loss or
XX CC weight maintenance required for purely cosmetic purposes.

SQ Sequence 839 AA;

Query Match 99.4%; Score 4337; DB 18; Length 839;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICOKFCVLLHWEFIYVITAFNLSPYITPWRFKLSMPPNSTYDFLLPAGLSKNTS 60

DB 1 micokfcvllhwefiyvitafnlspytprwfrklscmpnstydfllpaglskntsn 60

QY 61 NGHYETAPEKFNSSGTHFNSLKTTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120

DB 61 ngyetavepkfnssgthfnslnkttfhccfrseodrnscldadniegkftvstvnslvf 120

QY 121 QOIDANNIQCWLKGLDKLFCYVESLFRNLYNYKVHLLYVLPVLEDSPLVPQKGS 180

DB 121 qqidanwniqcwkglklfcyveslfrnlynykvhllylvpvledsplvpqkgs 180

QY 181 FQMVHCNCSVHECCCECLVPVPTAKLNDTLMLCKITSGGVIQSPPLMSVQPINNVKPDPP 240

DB 181 fgmvhcnscvheccceclvpvptaklndtlmlckitsggviqspplmsvqpinmvkpdpp 240

QY 241 LGLHMEITDDGNLKSWSPPPLVPFPLOQYQYKSENSTTVIRADKIVSATSLVDSILP 300
 Db 241 lglhmeitddgnlkswsppplvpfploqyqyksesttviradkivsatsllvdsilp 300
 QY 301 GSSYEQVQVRKRLDGPGLTWSWSTPRVFTTQDVVFPFKILTSVGSNVPFHCYKKNKI 360
 Db 301 gssyeqvqvrkrlldgpgltwsdstprvfttdqvfvfpfkiltsvgnsvfchcykknki 360
 QY 361 VPSKEIVWMNLAEKIPQSQYDVVSDHVSQVTFPFLNETKPRGKFTYDAVYCCNEHECHH 420
 Db 361 vpskeiivwmnlakeipqsgdydvvsdhsvskvtfnlnetkprgkftdyavycnehechh 420
 QY 421 RYAEIYVIDVWINISCTDGYLTWTCRWSTSTQSLAESTLQRLYHRSSLYCSDIPSIIH 480
 Db 421 ryaeliyvidvwiniscetdgyltktrwststqslaeestlqrlhrsslycsdipsih 480
 QY 481 PTSEPKDCYLQSDGFYECIFQPIFLLSGYTWIRINHSLSGLDPPPTCVLPDSVVKPLPP 540
 Db 481 ptsepkdcylqsdgyfecifqpfllsgytwirinhslsgldppptcvlpdsvvkplpp 540
 QY 541 SSVKAEITINTGLLKISWEKVPFPENNLOFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600
 Db 541 ssvkaeitintglklswekvpfpennlofqirylsgskevqwmvevydaksksvslpv 600
 QY 601 PDLCAVAVQVRCRLDGLGYWSNWPATVVMNDIKVPHRGPFWRINGDTWKKKNV 660
 Db 601 pdlcavavqvrclrdglgywsnwpayvvmndikvphrgpfrwringdwtwkkknv 660
 QY 661 TLLWKLKNDLSGQVRYVNIHNTSCNGTWSGSDVGNHRTFTFLWTQAHVTVLAINSI 720
 Db 661 tllwklkndlsqgyryvnihtscngtwsedvgnhrtftflwtqahtvtvlainsi 720
 QY 721 GASVANENLTFSPWMSKVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 780
 Db 721 gasvanenltfswpmskvnivqslasayplnsscvivswilspdyklymyfiewknlnd 780
 QY 781 GEIKWLRTSSSVKKYVINGKF 801
 Db 781 geikwlrtsssvkkyvindhf 801

RESULT 3
 AAW24052
 ID AAW24052 standard; Protein: 896 AA.
 XX
 AC AAW24052;
 XX
 DT 17-MAR-1998 (first entry)
 XX
 DE Human WSX receptor variant 6.4.
 XX
 KW Human; WSX receptor; variant 6.4; identification; purification;
 KW ligand; activator; antibody; agonist; proliferation; obesity;
 KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;
 KW Type II diabetes; polycystic ovarian disease;
 KW cardiovascular disease; osteoarthritis; dermatological disorder;
 KW hypertension; insulin resistance; hypercholesterolaemia;
 KW hypertriglyceridaemia; cancer; cholelithiasis.
 XX
 OS Homo sapiens.
 XX
 PN W09725425-A1.
 XX
 PD 17-JUL-1997.
 XX
 PF 07-JAN-1997; 97WO-US00325.
 XX
 PR 20-JUN-1996; 96US-0667197.
 PR 08-JAN-1996; 96US-0585005.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;

PI Rodrigues ML;
 XX WPI; 1997-372864/34.
 DR N-PSDB; AAT85576.
 XX
 PT WSX receptor and related antibodies and ligands - used to develop
 PT products for diagnosis and therapy, e.g. for improving
 PT haematopoiesis or for treating tumours
 XX
 PS Claim 2; Pages 86-89; 219pp; English.
 XX
 CC The present sequence is the human WSX receptor variant 6.4,
 CC which can be used to identify and purify ligands and activators.
 CC An anti-WSX receptor antibody can be used as an agonist to activate
 CC the WSX receptor, leading to enhanced proliferation or
 CC differentiation of a cell expressing the WSX receptor. It can also
 CC be used to decrease body weight and/or fat-depot weight and/or food
 CC intake in an obese mammal. WSX receptor ligands can be used to
 CC enhance proliferation or differentiation of lymphoid, myeloid or
 CC erythroid blood cell lineages. This is useful when a mammal,
 CC especially a human, is suffering from decreased blood cell levels,
 CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone
 CC marrow transplantation therapy. It can also be used to repopulate
 CC blood cells in a mammal. The products can also be used to treat,
 CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,
 CC polycystic ovarian disease, cardiovascular diseases,
 CC osteoarthritis, dermatological disorders, hypertension, insulin
 CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
 CC and cholelithiasis.
 XX
 SQ Sequence 896 AA;

Query Match 99.4%; Score 4337; DB 18; Length 896;
 Best Local Similarity 99.8%; Pred. No. 0;

Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIVYITAFNLSPYDITPWRFKLSCHMPNPNSTYDYPELLAGLSKNTSNS 60
 Db 1 micqkfcvllhwefiyvitaflnlsyptpwrfrklschmpnpsnydyfllpaglskntns 60
 QY 61 NGHYETAPEPKFNSGTHFNSLKTTFHCGRSEODRNCISLCADNIEGKTFVSNVSLVF 120
 Db 61 nghyetapepkfnsgthfnslkttfhcgrseodrnscslcadniegkftvsnvslvf 120
 QY 121 QQIDANWNIQCLWKGLKLFICYVESLFLKFLFRNYKVLHLYLPEVLEDSPVLPQKGS 180
 Db 121 qqidanwniqclwkglklficyveslflkflfrnykvhllylpevledsplvpqkgs 180
 QY 181 FQVHNCNSVHECCCECLVPVPTAKLNDTLMLCKITSGGVIFOSPLMSVQPINVKRPDPP 240
 Db 181 fqvhncnsvehccceclvpvptaklndtlmlckitsggvifosplmsvqipnvrkpdpp 240
 QY 241 LGLHMEITDDGNLKSWSPPPLVPFPLOQYQYKSENSTTVIRADKIVSATSLVDSILP 300
 Db 241 lglhmeitddgnlkswsppplvpfploqyqyksesttviradkivsatsllvdsilp 300
 QY 301 GSSYEQVQVRKRLDGPGLTWSWSTPRVFTTQDVVFPFKILTSVGSNVPFHCYKKNKI 360
 Db 301 gssyeqvqvrkrlldgpgltwsdstprvfttdqvfvfpfkiltsvgnsvfchcykknki 360
 QY 361 VPSKEIVWMNLAEKIPQSQYDVVSDHVSQVTFPFLNETKPRGKFTYDAVYCCNEHECHH 420
 Db 361 vpskeiivwmnlakeipqsgdydvvsdhsvskvtfnlnetkprgkftdyavycnehechh 420
 QY 421 RYAEIYVIDVWINISCTDGYLTWTCRWSTSTQSLAESTLQRLYHRSSLYCSDIPSIIH 480
 Db 421 ryaeliyvidvwiniscetdgyltktrwststqslaeestlqrlhrsslycsdipsih 480
 QY 481 PTSEPKDCYLQSDGFYECIFQPIFLLSGYTWIRINHSLSGLDPPPTCVLPDSVVKPLPP 540
 Db 481 ptsepkdcylqsdgyfecifqpfllsgytwirinhslsgldppptcvlpdsvvkplpp 540

QY 541 SSVKAEITINIGLTKISWEKPVFPENNLOFOIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600
 DB 541 ssvkaeitinigllkswepfpennlqfiryglsgkevqwmkvevydaaksksvslpv 600
 QY 601 PDLCAVAVQVRCKRLDGLGYWSNPNAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
 DB 601 pdlcavayavrcrkldgldgywsnwnpaytvvmdikvpmrgpewfwiingdtmkkeknv 660
 QY 661 TLLWKLPMKNDLSLCSVQRYVINNHHTSCNGTWSESDVGNHRTFTLWTEQAHVTVVLAINSI 720
 DB 661 tllwklpmkndslcsvqrvyvinhhtscngtwseadvgnhrtftlwteqahvtvvlainsi 720
 QY 721 GASVANFNLTFSWPMKKNVIVQSLAYPLNSSCVIVSWILSPDYDKLWYFIIEWKNLNED 780
 DB 721 gasvanfnltfswpmkknvqvslaysplnsscvivswilspdydklmyfielwknlned 780
 QY 781 GEIKWLRISSSVKYYIHGKF 801
 DB 781 geikwlriissvskyyihdhf 801

RESULT 4
 AAW24053
 ID AAW24053 standard; Protein; 923 AA.
 AC AAW24053;
 DT 17-MAR-1998 (first entry)
 DE Human WSX receptor variant 12.1.
 KW Human; WSX receptor; variant 12.1; identification; purification;
 KW ligand; activator; antibody; agonist; proliferation; obesity;
 KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;
 KW Type II diabetes; polycystic ovarian disease;
 KW cardiovascular disease; osteoarthritis; dermatological disorder;
 KW hypertension; insulin resistance; hypercholesterolaemia;
 KW hypertriglyceridaemia; cancer; cholelithiasis.
 XX Homo sapiens.
 OS
 XX WO9725425-A1.
 XX 17-JUL-1997.
 PD
 XX 07-JAN-1997; 97WO-US00325.
 XX 20-JUN-1996; 96US-0667197.
 PR 08-JAN-1996; 96US-0585005.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Bennett B, Carter PJ, Chlang NY, Kim KJ, Matthews W;
 PI Rodrigues ML;
 PI
 XX WPI; 1997-372864/34.
 DR N-PSDB; AAT85577.
 XX
 PT WSX receptor and related antibodies and ligands - used to develop
 PT products for diagnosis and therapy, e.g. for improving
 PT haematopoiesis or for treating tumours
 XX
 PS Claim 2; Pages 89-93; 219pp; English.
 XX
 CC The present sequence is the human WSX receptor variant 12.1,
 CC which can be used to identify and purify ligands and activators.
 CC An anti-WSX receptor antibody can be used as an agonist to activate
 CC the WSX receptor, leading to enhanced proliferation or
 CC differentiation of a cell expressing the WSX receptor. It can also
 CC be used to decrease body weight and/or fat-depot weight and/or food
 CC intake in an obese mammal. WSX receptor ligands can be used to
 CC enhance proliferation or differentiation of lymphoid, myeloid or
 CC erythroid blood cell lineages. This is useful when a mammal,

CC especially a human, is suffering from decreased blood cell levels,
 CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone
 CC marrow transplantation therapy. It can also be used to repopulate
 CC blood cells in a mammal. The products can also be used to treat,
 CC e.g. neoplastic disorders, arteriosclerosis, type II diabetes,
 CC polycystic ovarian disease, cardiovascular diseases,
 CC osteoarthritis, dermatological disorders, hypertension, insulin
 CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
 CC and cholelithiasis.
 XX
 XX Sequence 923 AA;

Query Match 99.4%; Score 4337; DB 18; Length 923;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICOKFCVLLHWEFIYVITAFNLSYPITPWRFKLSCMPNSTDYDFLLPAGLSKNTS 60
 DB 1 micokfcvllhwefiyvitafnlsypitpwrfklsmpnstdydfllpaglsknts 60
 QY 61 NGHYTEAVPEKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLACADNIEGKTEVSTVNSLVP 120
 DB 61 nghyetavpekfnsstgthfnslnskttfhccfrseqdrncslcadniegkfstvnslvf 120
 QY 121 QQIDANWNTQCLWKGDLKLFICYVESLFKNLFRNRYKVLHLYLPEVLEDSPLVPQKGS 180
 DB 121 qqldanwnlqclwkgdlklicyveslfknlfrnrykvhllylpevledsplvpqkgs 180
 QY 181 FOMVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGGVIFQSPMLSVQPINMWKPDPP 240
 DB 181 fomvhcnscsvheccclvpvptaklndtlmlclkitsggvifqspmlsvqipinmwkpdpp 240
 QY 241 LGLHMEITDDGNLKITSWSSPPLVPPPLQYQVKYSENSTTVIREADKIVSATSLVDSILP 300
 DB 241 lglhmeitddgnlkwssppplvpplqyqvkyseusttvireadkivsatslvsilp 300
 QY 301 GSSYEYQVRGKRLDGGPGIWSDMSTPRVFTQDVIYFPPKILTSVGSNSVSHCIYKKNKI 360
 DB 301 gssyeyvrgkrldgpgiwsdwtprvftqdviyfpfpkiltsvgsnsvshciykenki 360
 QY 361 VPSKETVMMNLAEKIPQSDYDVSDHVSQVTFNNLNETKPRGKETYDAVYCCNEHECHH 420
 DB 361 vpskeivmmnlakqipsgdydvshvskvtfnnlnetkprgktydavyccnehechh 420
 QY 421 RYAELYVIDVININISCEYDGLTKMTCRWSTSTIOSLAESTLQLRVHBSLYCSDIPSILH 480
 DB 421 ryaelyvidvininiscedygltkmtcrwststioslaestlqlrvhbslycsdipsilh 480
 QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSIGSLDSDPTCVLPDSVVKPLPP 540
 DB 481 pisepkdcylqsdgfyecifqipifllsgytmwirinhslgslsdptcvlpdsvvkplpp 540
 QY 541 SSVKAEITINIGLTKISWEKPVFPENNLOFOIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600
 DB 541 ssvkaeitinigllkswepfpennlqfiryglsgkevqwmkvevydaaksksvslpv 600
 QY 601 PDLCAVAVQVRCKRLDGLGYWSNPNAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
 DB 601 pdlcavayavrcrkldgldgywsnwnpaytvvmdikvpmrgpewfwiingdtmkkeknv 660
 QY 661 TLLWKLPMKNDLSLCSVQRYVINNHHTSCNGTWSESDVGNHRTFTLWTEQAHVTVVLAINSI 720
 DB 661 tllwklpmkndslcsvqrvyvinhhtscngtwseadvgnhrtftlwteqahvtvvlainsi 720
 QY 721 GASVANFNLTFSWPMKKNVIVQSLAYPLNSSCVIVSWILSPDYDKLWYFIIEWKNLNED 780
 DB 721 gasvanfnltfswpmkknvqvslaysplnsscvivswilspdydklmyfielwknlned 780
 QY 781 GEIKWLRISSSVKYYIHGKF 801
 DB 781 geikwlriissvskyyihdhf 801

```

RESULT 5
AAW34499
ID AAW34499 standard; protein; 970 AA.
AC AAW34499;
XX
DT 18-MAR-1998 (first entry)
XX
DE Obesity receptor C protein.
XX
KW Obesity receptor; human; OB receptor; OB receptor/OB protein complex;
KW high blood lipid level; obesity; diabetes; high cholesterol level;
KW weight loss; therapy; weight maintenance.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 959 /label= "unknown"
FT /note= "encoded by stop codon"
XX
PN W09725424-AL.
XX
PD 17-JUL-1997.
XX
PF 02-JAN-1997; 97WO-US00128.
XX
PR 31-DEC-1996; 96US-0774414.
PR 04-JAN-1996; 96US-0582825.
XX
PA (AMGE-) AMGEN INC.
XX
PI Chang M, Fletcher FA, Welcher AA;
XX
DR WPI; 1997-384981/35.
DR N-PSDB; AAT98530.
XX
PT Obesity protein receptor(s) and related DNA - used to treat weight
PT disorders, e.g. obesity, diabetes and high cholesterol or blood
PT lipid levels
XX
PS Claim 2; Page 72; 151pp; English.
XX
CC This sequence represents the obesity (OB) receptor C protein. This
CC sequence has one or more of the biological properties of naturally
CC occurring OB receptor protein. The OB receptor proteins and OB
CC receptor/OB protein complexes are used for the treatment of obesity,
CC diabetes, high blood lipid levels and high cholesterol levels. The
CC proteins may also be used to treat an individual for weight loss or
CC weight maintenance required for purely cosmetic purposes.
XX
SQ Sequence 970 AA;

Query Match 99.4%; Score 4337; DB 18; Length 970;
-Best Local Similarity 99.8%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFLVITAFNLSPITPWRFKLSMPNPNSTYDFLLPAGLSKNTS 60
DB 1 micqkfcvllhweflyvitafnlspitpwrfrklsmpnpnstydyflilpaglsknts 60
QY 61 NGHYETAPEKFNSSGTHFSNLSKTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
DB 61 nghyetavepkfnssgthfsnlskttfhccfrseqdrnscslcadniegktfvstvnslvf 120
QY 121 QQIDANNIQCWLKGLDLFCYVESLFLKMLFRNYKYVHLLYVLPEVLEDSPLVPQKGS 180
DB 121 qqidanwniqcwlkglldlfcyveslflkmlfrnykyvhllylvlevedsplvpqkgs 180
QY 181 FQWVHCNCSVHECECLVPVPTAKLNDTLMLKITSGGVIFQSPMLSVQPINNVKPDPP 240
DB 181 fqmvhcnscvhececlvpvptaklndtllmclkitsggvifqspmlsvqpinmvkpdpp 240

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DB 181 fqmvhcnscvhececlvpvptaklndtllmclkitsggvifqspmlsvqpinmvkpdpp 240
QY 241 LGLHMEITDDGNLKIWSNPPPLVPFPLQYQVYKYSSENSTVIREADKIVSATSLVDLSLP 300
XX 241 lglhmeitddgnlkiwsnppplvpfpfqyqvkysensttvi readkivsatllvdsilp 300
DB 241 lglhmeitddgnlkiwsnppplvpfpfqyqvkysensttvi readkivsatllvdsilp 300
QY 301 GSSYEVOVRGRKLDGPGIWSDMSTPRVFTTQDVIFPPKILTSVGSNVSFHCYKKNKI 360
DB 301 gssyevovrgrkldpgiwsdmstprvfttqdvifppkiltsvgsnvsfchcykknki 360
QY 361 VPSKEIYVMNNAEKIPQSOYDVVSDHVSVTFFNLNETPKRGKFTYDAVYCCNEHECHH 420
DB 361 vpskeiyvmnnlaekipqsoydvvsvdhvsvtfnnlnetprgkftdyavycnehechh 420
QY 421 RYAEIYVIDVINISCTDGYLTMTCTRWSTSTTQSLAESTLQLRHRSLSYSDIPSIIH 480
DB 421 ryaeliyvidviniscetdgyltkmtcrwststtqslaeestlqlryhrsslycsdipsih 480
QY 481 PISEPKDCYLQSDGFYECIFQIFLLSGYTMWIRINHSLSLSDSPPTCVLPDSVVKPLPP 540
DB 481 pisepkdcylqsdgfyecifqifllsgytmwirinhsldspptcvi pdsvvkplpp 540
QY 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600
DB 541 ssvkaeitinigllkiswekvpfpennlqfairyglsgkevqwmvevydaksksvslpv 600
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNPNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
DB 601 pdlcavyavqvrckrldglgywsnspaytvvmdikvpmrgpefwriingdtmkkeknv 660
QY 661 TLLWKPLMKNDLSICSVORYVINHHTSCNGTWSVDGNGHRTFTFLWTEQAHVTVVLAINSI 720
DB 661 tllwkpmlkndlsicsvoryvinhhtscngtwsedvgnhtkftflwteqahvtvvlainsi 720
QY 721 GASVANENLTFSPMSKVNIVQSLSAYPLNSCVIVSWILSPSDYKIMYFTIEWKNLNE 780
DB 721 gasvanenltsfpmkskvnivqslsayplnsscvivswilspdsykimyftiewknlned 780
QY 781 GEIKWLRISSSVKRYIHKGF 801
DB 781 geikwlrisssvkkyyihdhf 801

RESULT 6
AAW34497
ID AAW34497 standard; protein; 972 AA.
XX
AC AAW34497;
XX
DT 18-MAR-1998 (first entry)
XX
DE Obesity receptor A protein.
XX
KW Obesity receptor; human; OB receptor; OB receptor/OB protein complex;
KW high blood lipid level; obesity; diabetes; high cholesterol level;
KW weight loss; therapy; weight maintenance.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 897 /label= "unknown"
FT /note= "encoded by stop codon"
FT Misc-difference 919 /label= "unknown"
FT /note= "encoded by stop codon"
FT Misc-difference 925 /label= "unknown"
FT /note= "encoded by stop codon"
FT Misc-difference 939 /label= "unknown"
FT /note= "encoded by stop codon"
FT Misc-difference 948 /label= "unknown"
FT /note= "encoded by stop codon"

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FT /label= unknown
FT /note= "encoded by stop codon"
FT Misc-difference 952
FT /label= unknown
FT /note= "encoded by stop codon"
FT Misc-difference 971
FT /label= unknown
FT /note= "encoded by stop codon"
XX

W09725424-AL.

17-JUL-1997.

02-JAN-1997; 97WO-US00128.

31-DEC-1996; 96US-0774414.

04-JAN-1996; 96US-0582825.

(AMGE-) AMGEN INC.

Chang M, Fletcher FA, Welcher AA;

WPI; 1997-384981/35.

N-PSDB; AAT98528.

Obesity protein receptor(s) and related DNA - used to treat weight disorders, e.g. obesity, diabetes and high cholesterol or blood lipid levels

Claim 1; Page 64; 151pp; English.

This sequence represents the obesity (OB) receptor A protein. This sequence has one or more of the biological properties of naturally occurring OB receptor protein. The OB receptor proteins and OB receptor/OB protein complexes are used for the treatment of obesity, diabetes, high blood lipid levels and high cholesterol levels. The proteins may also be used to treat an individual for weight loss or weight maintenance required for purely cosmetic purposes.

Sequence 972 AA;

Query Match 99.4%; Score 4337; DB 18; Length 972;
Best Local Similarity 99.8%; Pred. NO. 0;
Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPTIPWRFKLSMPNSTYDFLLPAGLSKNTS 60
Db 1 micqkfcvllhwefiyvitafnlsyptipwrfklsmpnstydfllpaglsknts 60
QY 61 NGHYETAVEPKNSGTHFSNLSKTTFFHCCFRSEQDRNCSLCADNTEGKTFVSTVNSLVF 120
Db 61 nghyetavepkfnsqthfsnlskttffhccfrseqdrncslcadniegkftvstvnslvf 120
QY 121 QIDANWNIQCKLKGDLKLFICYVESLKNLERNYKVVHLLVLPVLEDSPLVPQKS 180
Db 121 qidanwnlqcklkgdlklficyveslknlnrnykvhllylvpvleedsplvpqks 180
QY 181 FQVHNCNSVHECCCLVPVPTAKLNDTLLMCLKITSGGVIFQSPMLSVQPINMVKPDPP 240
Db 181 fqmvhncnsvehccclvpvptaklndtllmclkitsggvifqspmlsvqpinmvpdpdp 240
QY 241 LGLHMEITDGNLKIWSGSPPLVPFPLOQVYKSENSTTVIREADKIVSATSLLVDSILP 300
Db 241 lglhmeitdgnlkiwsdspplvpfploqvkyseussttvireadkivsatsllvdsilp 300
QY 301 GSSYEVOVREGKRLDGGTWSNDSTVRFTTQDIYFPKILTSVGSNSVHFHCKENKI 360
Db 301 gssyeovvregkrlldggtwsndstvrfttqdiyfppkiltsvgsnsvfhfckkenki 360
QY 361 VPSKEIVWMNLAEKIPQSOYDWSHDVSKVTFNNLNETKPRGFTYDAVYCCNEHECHH 420
Db 361 vpskelvwmnlakelpsqdyvshsvskvtfnnlnetkprgftdyavycnehechh 420

QY 421 RYAELVYVIDVNIINISCTDGYLTCKMTCRWSTSTIQSLAESTLQLRVHRSSLYCSDIPSIH 480
Db 421 ryaelvyvidvniiniscetdgyltckmcrwststiqslaestlqlyrhrsslycsdipslh 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGTYTMIIRINHSLSGSDSPPTCVLPDSVVKPLPP 540
Db 481 pisepkdcylqsdgfyecifqpifllsgytmwirinhsldspptcvlpdsvvkplpp 540
QY 541 SSVKAELTINIGLLKISWEKPPENNLOFQIRYGLSGREVQHKMYEVDKAKSVSLPV 600
Db 541 ssvkaeltinigliskiswekvpennlqfiryglsgrevqhkmyevdydaksksvslpv 600
QY 601 PDLCAVYAVQVRCRLDGLGYNSNPNAYTVVMDIKVPMRGPEFWRIINGDPMKKEKNV 660
Db 601 pdlcavyavqvrckrlldggywnsnpnaytvvmdikvpmrgpefwrlingdmkkekknv 660
QY 661 TLLWKPLMKNDSLCVQRYVINHTSCNGTWSGVNHTKFTFLMTEQAHVTVLAINSI 720
Db 661 tllwkplmkndslcsqrvyvinhtscngtwsedvgnhckftflwteqahvtvlnainsi 720
QY 721 GASVANFLTFESWPMKSNVIVQSLAYSAYPLNSCIVYVSWILSPSDYKLMYFIIEWKNLNE 780
Db 721 gasvanfltfeswpmksnvlvqslaysayplnscvlyvswilspdyklymfiiewknlne 780
QY 781 GEIKWLIRISSSVKKYVYHGKF 801
Db 781 geikwlirissvkkyyihdhf 801

RESULT 7

AAW34498
ID AAW34498 standard; protein; 999 AA.

XX AAW34498;

XX 18-MAR-1998 (first entry)

DE Obesity receptor B protein.

KW Obesity receptor; human; OB receptor; OB receptor/OB protein complex;
KW high blood lipid level; obesity; diabetes; high cholesterol level;
KW weight loss; therapy; weight maintenance.

OS Homo sapiens.

XX Key Location/Qualifiers
FT Misc-difference 905 /label= unknown
FT Misc-difference 933 /note= "encoded by stop codon"
FT Misc-difference 971 /label= unknown
FT Misc-difference 971 /note= "encoded by stop codon"
FT Misc-difference 988 /label= unknown
FT Misc-difference 988 /note= "encoded by stop codon"
FT Misc-difference 988 /label= unknown
FT Misc-difference 988 /note= "encoded by stop codon"

W09725424-AL.

17-JUL-1997.

02-JAN-1997; 97WO-US00128.

31-DEC-1996; 96US-0774414.

04-JAN-1996; 96US-0582825.

(AMGE-) AMGEN INC.

Chang M, Fletcher FA, Welcher AA;

DR WPI: 1997-384981/35.
DR N-PSDB; AAT98529.

XX Obesity protein receptor(s) and related DNA - used to treat weight
PT disorders, e.g. obesity, diabetes and high cholesterol or blood
PT lipid levels

XX Claim 2; Page 68; 151pp; English.

XX This sequence represents the obesity (OB) receptor B protein. This
CC sequence has one or more of the biological properties of naturally
CC occurring OB receptor protein. The OB receptor proteins and OB
CC receptor/OB protein complexes are used for the treatment of obesity,
CC diabetes, high blood lipid levels and high cholesterol levels. The
CC proteins may also be used to treat an individual for weight loss or
CC weight maintenance required for purely cosmetic purposes.

XX Sequence 999 AA;

Query Match 99.4%; Score 4337; DB 18; Length 999;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSPYTPWRKRLSCMPNSTDYDFLLPAGLSKNTSNS 60
DB 1 micqkfcvllhwefiyvitafnlspypwrfklscompnstydyflpagskntns 60
QY 61 NGHYETAPEKFNSSGTHFNLSKTTFFHCCFRSEQRNCSLCADNIEGRTFVSTVNSLVF 120
DB 61 nghyetapekfnssthfnlskttffhccfrseqrncslcadniegkrtfstvnslvf 120
QY 121 QQIDANNIOCLWGLDGLKFLICVSESLFKNLFNRYNKKVHLLYVLPEVLEDSPLVPQKS 180
DB 121 qqidannioclwglldglkflfcvsefslfknlfnyknkvhllylvlevedsplvpqks 180
QY 181 FQMVHNCVSHECCVCECIVPPTAKLNDTLMLCKITSGGVIFQSPMSVQPINNVKPDPP 240
DB 181 fqmvhncvsheccvceci v p p t a k l n d t l m l c k i t s g g v i f q s p m s v q p i n n v k p d p p 240
QY 241 LGLHMEITDGNLKIWSPPPLVPFPLOQYQVYSENSTTVIREADKIVSATSLLVDSILP 300
DB 241 lglhmeitdgnlkiwsppplvpfploqyqvysensttvireadkivsatsllvdsilp 300
QY 301 GSSYEVQVRGKRLDGPGLKSDWSTPRVETQDVIYEPKILTSGVSNVSPHCYKKNKI 360
DB 301 gssyevqvrgrldgpglksdwstprvettodviyepkiltsgvsnvshciykkenki 360
QY 361 VPSKEIYVWNNLAEKIPQSYQYDVVSDHVSQVTFPFLNETKPRGKFTYDAVYCCNEHECHH 420
DB 361 vpskelvwmnlaekipqsgydvvsdhvskvtfpflnetkprgkfydavyccnehechh 420
QY 421 RYAEIYVIDVNNISCEGTGTLTKTCRWSTSTIQSLAESTLQLRYHRSLSYCDIPSIH 480
DB 421 ryaeliyvidvnniscedgtl tk t c r w s t s t i q s l a e s t l q l r y h r s l y c d i p s i h 480
QY 481 PISEPKDCYLOSGDFECLFQPTFLLSGYTMMIRINHSLGSLDSPCTCVLPDSVVRPLPP 540
DB 481 pisepkdcylsgdfecfqlpftllsgytmwirinhslgsldspctcvlpdsvvrplpp 540
QY 541 SSVKAEITINIGLLKISWEKPPVPPENNLQFQIRYGLSGKEVQWKMVEYVDKSKVSLPV 600
DB 541 ssvkaeitinigllkswkppvp p p p e n n l q f q i r y g l s g k e v q w k m v e y v d a k s k v s l p v 600
QY 601 PDLCAVAVQVRCKRLDGLGYSWNSNPATVVMVDIKVPMRGPEFWRIRIINGDTMKKEKNV 660
DB 601 pdlcavavqvrckrl d g l g y s w n s n p a t v v m v d i k v p m r g p e f w r i r i n g d t m k k e k n v 660
QY 661 TLWKPLMKNDLSLCSQRYVINHTSCNGTWSVDGNHKKFTFLWTEQAHTVTVLAINSI 720
DB 661 tlwkp l m k n d s l c s q r y v i n h t s c n g t w s v d g n h k k f t f l w t e q a h t v t v l a i n s i 720
QY 721 GASVANFNLTFSMPKSNVIVQSLSATYPLNSSCVIVSWILSPSDYKLMFYIEWKNLINED 780

DB 721 gasvanfnltfswpmkvnivqslsatyplnsscvivswilspdyk l m f y i e w k n l i n e d 780

QY 781 GEIKWLRISSVKKYIYHGKF 801

DB 781 geikwlrisssvkkyyihgkf 801

RESULT 8

AAW24051

ID AAW24051 standard; Protein; 1165 AA.

XX

AC AAW24051;

XX

DT 17-MAR-1998 (first entry)

XX

DE Human WSX receptor variant 13.2.

XX

KW Human: WSX receptor; variant 13.2; identification; purification;
KW ligand; activator; antibody; agonist; proliferation; obesity;
KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;
KW Type II diabetes; polycystic ovarian disease;
KW cardiovascular disease; osteoarthritis; dermatological disorder;
KW hypertension; insulin resistance; hypercholesterolaemia;
KW hypertriglyceridaemia; cancer; cholelithiasis.

XX Homo sapiens.

OS

PN WO9725425-A1.

XX

PD 17-JUL-1997.

XX

PF 07-JAN-1997; 97WO-US00325.

XX

PR 20-JUN-1996; 96US-0667197.

XX

PR 08-JAN-1996; 96US-0585005.

XX

PA (GETH) GENENTECH INC.

XX

PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;

PI Rodrigues ML;

XX

WPI: 1997-372864/34.

DR

N-PSDB; AAT85575.

XX

WSX receptor and related antibodies and ligands - used to develop

products for diagnosis and therapy, e.g. for improving

haematopoiesis or for treating tumours

PT

XX Claim 2; Pages 81-85; 219pp; English.

PS

XX The present sequence is the human WSX¹ receptor variant 13.2,
CC which can be used to identify and purify ligands and activators.
CC An anti-WSX receptor antibody can be used as an agonist to activate
CC the WSX receptor, leading to enhanced proliferation or
CC differentiation of a cell expressing the WSX receptor. It can also
CC be used to decrease body weight and/or fat-depot weight and/or food
CC intake in an obese mammal. WSX receptor ligands can be used to
CC enhance proliferation or differentiation of lymphoid, myeloid or
CC erythroid blood cell lineages. This is useful when a mammal,
CC especially a human, is suffering from decreased blood cell levels,
CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone
CC marrow transplantation therapy. It can also be used to repopulate
CC blood cells in a mammal. The products can also be used to treat,
CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,
CC polycystic ovarian disease, cardiovascular diseases,
CC osteoarthritis, dermatological disorders, hypertension, insulin
CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
CC and cholelithiasis.

XX Sequence 1165 AA;

SQ

Query Match	99.4%; Score 4337; DB 18; Length 1165;	Best Local Similarity 99.8%; Pred. No. 0;	Mismatches 799; Conservative 0; Gaps 0;
QY	1 MICQKFCVLLHWEFIYVITAFNLSYPTWPRFKLSMPNPNSTYDFLLPAGLSKNTSNS 60	1 micqkfcvllhwefiyvitafnlsyptwprfklsmpnpsnydfllpaglskntsns 60	
DB	1 micqkfcvllhwefiyvitafnlsyptwprfklsmpnpsnydfllpaglskntsns 60	1 micqkfcvllhwefiyvitafnlsyptwprfklsmpnpsnydfllpaglskntsns 60	
QY	61 NGHYETAVERKFNSSGTHFNSLKTTHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120	61 ngyetavepknssgthfnslnktthccfrseqdrcnscadniegkttfstvnslvf 120	
DB	61 ngyetavepknssgthfnslnktthccfrseqdrcnscadniegkttfstvnslvf 120	61 ngyetavepknssgthfnslnktthccfrseqdrcnscadniegkttfstvnslvf 120	
QY	121 QOIDANFNIOCWLGKDLKLFICVYESLFKNLFRNRYKVHLLYVLPVLEDSPLVPQKGS 180	121 qoidanfnioqwlkgdlklficyveslfknlfrynkvhlllylpevledsplvpqkgs 180	
DB	121 qoidanfnioqwlkgdlklficyveslfknlfrynkvhlllylpevledsplvpqkgs 180	121 qoidanfnioqwlkgdlklficyveslfknlfrynkvhlllylpevledsplvpqkgs 180	
QY	181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGGVIFQSPILMSVQPINMVKPDPP 240	181 fgmvhcnscsvheccclvpvptaklndtlmlckitsggvifqspilmsvqpinmvpkpp 240	
DB	181 fgmvhcnscsvheccclvpvptaklndtlmlckitsggvifqspilmsvqpinmvpkpp 240	181 fgmvhcnscsvheccclvpvptaklndtlmlckitsggvifqspilmsvqpinmvpkpp 240	
QY	241 LGHMEITDDGNLKIWSNPPLVPFPLOQYKVSNSSTTVIREADKIYSATSLVDSILP 300	241 lghmeitddgnlkiwsnpplvpfploqykvnssttvireadkiysatsslvdslp 300	
DB	241 lghmeitddgnlkiwsnpplvpfploqykvnssttvireadkiysatsslvdslp 300	241 lghmeitddgnlkiwsnpplvpfploqykvnssttvireadkiysatsslvdslp 300	
QY	301 GSSYEYQVGRKRLDGGIWSNSTPRVFTQDVIYPPPKILTSVGSNSVFHCIIYKKNKI 360	301 gssyeqvgrkrlldggiwsnstprvftqdvipppkiltsvgsnsvfhciykknki 360	
DB	301 gssyeqvgrkrlldggiwsnstprvftqdvipppkiltsvgsnsvfhciykknki 360	301 gssyeqvgrkrlldggiwsnstprvftqdvipppkiltsvgsnsvfhciykknki 360	
QY	361 VPSKEIVWMNLAEKIPQSOYDVSDVSHVSKVTFNNLTKPRGKTYDAVCCNEHECHH 420	361 vpskeivwmnlakipqsoydvsvshvskvtfnnltpkgktydavccnehechh 420	
DB	361 vpskeivwmnlakipqsoydvsvshvskvtfnnltpkgktydavccnehechh 420	361 vpskeivwmnlakipqsoydvsvshvskvtfnnltpkgktydavccnehechh 420	
QY	421 RYAEIVYDWNINISCTDGYITKMTCRWSTSTIQSLAESTLQLRHRSLSLYCSDIPSII 480	421 ryaeivydwninisctdgyitkmtcrwststiqslaeestlqlrhrslslycsdipsii 480	
DB	421 ryaeivydwninisctdgyitkmtcrwststiqslaeestlqlrhrslslycsdipsii 480	421 ryaeivydwninisctdgyitkmtcrwststiqslaeestlqlrhrslslycsdipsii 480	
QY	481 PISEKDCYLOSGDFEYECFQPIELLSGVTWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540	481 pisekdcylodsgdfeyecfqpilslsgvtwirinhslsdldspptcvlpdsvvklpp 540	
DB	481 pisekdcylodsgdfeyecfqpilslsgvtwirinhslsdldspptcvlpdsvvklpp 540	481 pisekdcylodsgdfeyecfqpilslsgvtwirinhslsdldspptcvlpdsvvklpp 540	
QY	541 SSVKABITINIGLLTSWEPKVPENNIFQIRYGLSGKEVQWKMVEYDAKSVSLPV 600	541 ssvkabitiniglltswekpvpennifqirylsglsgkevqwmveydaksvslpv 600	
DB	541 ssvkabitiniglltswekpvpennifqirylsglsgkevqwmveydaksvslpv 600	541 ssvkabitiniglltswekpvpennifqirylsglsgkevqwmveydaksvslpv 600	
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DB	601 pdlcavavqvrckrldglgyswnsnpaytvvmdikvpmrgpfefriingdtmkkeknv 660	601 pdlcavavqvrckrldglgyswnsnpaytvvmdikvpmrgpfefriingdtmkkeknv 660	
QY	661 TLWKPMLKNDISCSVORVIVNHHTSCNGTWSVDGNHTKFTFLWTQAHVTVLAINSI 720	661 tlwkpmlkndiscsvorvivnhhtscngtwsvdgnhtkftflwtqahvtvlainsi 720	
DB	661 tlwkpmlkndiscsvorvivnhhtscngtwsvdgnhtkftflwtqahvtvlainsi 720	661 tlwkpmlkndiscsvorvivnhhtscngtwsvdgnhtkftflwtqahvtvlainsi 720	
QY	721 GASVANFNLTFSWPMKSNVIVQSLAYSALPNSCVISVLSWILSPSDYKLMYFTIEWKLNED 780	721 gasvanfnltsfswpmksnvivqslaysalpnscvsvlswilspdyklmyftiewklned 780	
DB	721 gasvanfnltsfswpmksnvivqslaysalpnscvsvlswilspdyklmyftiewklned 780	721 gasvanfnltsfswpmksnvivqslaysalpnscvsvlswilspdyklmyftiewklned 780	
QY	781 GEIKWLIRISSSVKKYIYHNGKF 801	781 geikwlirissvkkyyihngkf 801	
DB	781 geikwlirissvkkyyihngkf 801	781 geikwlirissvkkyyihngkf 801	
RESULT	9		
AA13474	standard; Protein; 1165 AA.		
ID	AA13474		
AC	AA13474;		
XX			
DT	26-JUL-1999 (first entry)		
XX			
DE	Peptide Seq ID No: 4 of W09923493.		
XX			
XX	Leptin; phosphorylated leptin receptor; tyrosine phosphatase 1D; PTP-1D;		
XX	modulator; drug; weight loss; adiposity; hypertension; heart disease;		
KW	type II diabetes; cancer; AIDS; agriculture.		
XX	Homo sapiens.		
OS	W09923493-A1.		
PN	14-MAY-1999.		
XX	27-OCT-1998; 98WO-US22797.		
XX	26-OCT-1998; 98US-0178691.		
PR	31-OCT-1997; 97US-0961809.		
XX	(UYRQ) UNIV ROCKEFELLER.		
XX	Friedman JM, Li C;		
XX	WPI; 1999-327025/27.		
DR	N-PSDB; AAX55588.		
XX	Identifying modulators agents that modulate leptin activity		
PS	Disclosure; Page 77-84; 96pp; English.		
XX	The invention provides a method for identifying modulators of binding of a phosphorylated leptin receptor with tyrosine phosphatase 1D PTP-1D.		
CC	The method comprises: (a) contacting a tyrosine-985 phosphorylated		

```

Db 301 gssyevvrgkridgpgiwsdwtprvftqdvifppkiltsvgsnvsfchcykknk 360
QY 361 VPSKEIYWMNLAEKIQSOYDVVSDHVSQVTFENLTKPRGFTYDAVYCCNEHCHH 420
Db 361 vpskeiywmnlaekiqsdydvsvdhvskvtfnlnetkprgkftdyavycnehechh 420
QY 421 RYAEIYVIDVNIINISCTDGYLTKMTCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPS 480
Db 421 ryaeliyvidvniiniscetdgyltkmtcrwststiqslaestqlryhrsslycsdipsh 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSIGSLDSDPPCTCVLPDSVVRPLPP 540
Db 481 pisepkdcylqsdgfyecifqpfllsgytmwirinhsigslsdppctcvlpdsvvrplpp 540
QY 541 SSVKAEITINIGLTKISWEKPVFPENNLOFQIRYGLSGKEVQWKMVEYDAKSKVSLPV 600
Db 541 ssvkaeitinigltkiswekpvfpennlqfiryglsgkevqwmvevydaksksvslpv 600
QY 601 PDLCAVAVOVRKRLDGLGYWNSNPATVYMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 pdlcavavovrkrlldgloywnsnpatvymdikvpmrgpewfriingdtmkkeknv 660
QY 661 TLWKPMLKNDLSLCSVQRYVINHHTSCNGTWSGVNHTKFTLTWEOAHTVTVLAINSI 720
Db 661 tlwkpmlkndslcsvqryvinhhtscngtwsedvgnhtkftltwteqahvtvclainsi 720
QY 721 GASVANFNLTFSWPMKVNIVQSLAYPLNMSCVIVSWILSPDSQDKLMYFIIEWKNLNE 780
Db 721 gasvanfnltfswpmkvnivqslaysplnmscvivswilspdsqdklmfyiiewknlne 780
QY 781 GEIKWIRISSVKKYIHGKF 801
Db 781 geikwirissvkkyyihdhf 801

RESULT 10
AAW34500
ID AAW34500 standard; protein; 1220 AA.
XX AC AAW34500;
XX DT 18-MAR-1998 (first entry)
XX DE Obesity receptor D protein.
KW Obesity receptor; human; OB receptor; OB receptor/OB protein complex;
KW high blood lipid level; obesity; diabetes; high cholesterol level;
KW weight loss; therapy; weight maintenance.
XX OS Homo sapiens.
XX FH Key
XX FT Location/Qualifiers
XX FT Misc-difference 1...1165
XX FT /note= "encoded by AAT98531"
XX FT Misc-difference 1166
XX FT /label= unknown
XX FT /note= "encoded by stop codon"
XX FT Misc-difference 1169
XX FT /label= unknown
XX FT /note= "encoded by stop codon"
XX FT Misc-difference 1187
XX FT /label= unknown
XX FT /note= "encoded by stop codon"
XX FT Misc-difference 1207
XX FT /label= unknown
XX FT /note= "encoded by stop codon"
XX FT Misc-difference 1...1165
XX FT /note= "encoded by AAT98531"
XX PN W09725424-A1.
XX PD 17-JUL-1997.

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XX 02-JAN-1997; 97WO-US00128.
XX 31-DEC-1996; 96US-0774414.
PR 04-JAN-1996; 96US-0582825.
XX (AMGE-) AMGEN INC.
XX Chang M, Fletcher FA, Welcher AA;
XX WPI: 1997-384981/35.
DR N-PSDB; AAT98531.
XX Obesity protein receptor(s) and related DNA - used to treat weight
PT disorders, e.g. obesity, diabetes and high cholesterol or blood
PT lipid levels
XX Claim 31; Page 76; 151pp; English.
XX This sequence represents the obesity (OB) receptor D protein. This
CC sequence has one or more of the biological properties of naturally
CC occurring OB receptor protein. The OB receptor proteins and OB
CC receptor/OB protein complexes are used for the treatment of obesity,
CC diabetes, high blood lipid levels and high cholesterol levels. The
CC proteins may also be used to treat an individual for weight loss or
CC weight maintenance required for purely cosmetic purposes.
XX Sequence 1220 AA;
SQ
Query Match 99.4%; Score 4337; DB 18; Length 1220;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MICOKFCVLLHWEFIYVITAENLSYPITPWRFKLSCMPNSTYDYFLLPAGLSKNTS 60
Db 1 micokfcvllhwefiyvitafnlspitpwrklscompnstydyfllpaglsknts 60
QY 61 NGHYTEAVBPKFNSSGTHFSNLSKTTFFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 nghyetavebpfkfnssgthfnskskttffhccfrseodrnscslcadniegkftvstvnslvf 120
QY 121 QOIDANWNTQCLWKGDLKLFICYVSLFKNLFRNRYKVVHLLYVLPVLEDSPLVPQKGS 180
Db 121 qqoidanwnlqcvlkgdlkficyveslfknlfrnykvhlllyvlpvleedsplvpqkgs 180
QY 181 FOMVHCNCSVHECCCECLVPVPTAKLNDTLMLCLTKTSGGVIFQSPILMSVQPINMVKPDP 240
Db 181 fgmvhcnscsvheccceclvpvptaklndtlmlcltktsggvifqspilmsvqipnmvkpdp 240
QY 241 LGLHMEITDDGNLKISWSSPLVPFPLOQYKYSENSTTVIREADKIYSATSLLVDSILP 300
Db 241 lglhmeitddgnlkiwssplvpfploqykysesttvireadkiysatsllvdsilp 300
QY 301 GSSYEVQVRGKRLDGPGLWSWSDSTPRVFTTQDVIFPPPKILTSVGSNVSFHCYKKNKI 360
Db 301 gssyevqvrgrkrlldgpglwsdswstprvfttqdvifppkiltsvgsnvsfchcykknki 360
QY 361 VPSKEIYWMNLAEKIQSOYDVVSDHVSQVTFENLTKPRGFTYDAVYCCNEHCHH 420
Db 361 vpskeiywmnlaekiqsdydvsvdhvskvtfnlnetkprgkftdyavycnehechh 420
QY 421 RYAEIYVIDVNIINISCTDGYLTKMTCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPS 480
Db 421 ryaeliyvidvniiniscetdgyltkmtcrwststiqslaestqlryhrsslycsdipsh 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSIGSLDSDPPCTCVLPDSVVRPLPP 540
Db 481 pisepkdcylqsdgfyecifqpfllsgytmwirinhsigslsdppctcvlpdsvvrplpp 540
QY 541 SSVKAEITINIGLTKISWEKPVFPENNLOFQIRYGLSGKEVQWKMVEYDAKSKVSLPV 600
Db 541 ssvkaeitinigltkiswekpvfpennlqfiryglsgkevqwmvevydaksksvslpv 600

```

QY 601 PDLCAVAVQVRCKRLDGLGYWSNWNPNAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
 DB 601 pdlcavavqvrckrlidggywsnwnpnaytvvmdikvpmrgpefwrriingdtmkkeknv 660
 QY 661 TLKWKPLMKNDLSQVQRYVINHTSCNGTWSQEDVGNHTKFTFLWTEQAHVTVLAINSI 720
 DB 661 tllwkpmlkndlsqvrqyvinhtscngtwsedvgnhktftflwteqahvvtvlainsi 720
 QY 721 GASVANFNLTFSWPMKSNVIVQSLASAYPLNSCVIVSWILSPSDYKLMYFIIEWKNLNED 780
 DB 721 gasvanfnltfswpmksnvivqslasayplnscvsvilswilspdyklymfiiewknlnd 780
 QY 781 GEIKWLRISSVKKYYIHGKF 801
 DB 781 geikwlriissvkkyyihdhf 801

RESULT 11

AAW50003
 ID AAW50003 standard; Protein; 896 AA.

XX
 AC AAW50003;

XX
 DT 11-JUN-1998 (first entry)

XX
 DE Human OB-R variant Form 3.

XX
 KW Detection; defective obese protein receptor; defective OB-R; human;
 KW defective leptin receptor; variant Form 3; infertility.

XX
 OS Homo sapiens.

XX
 PN WO9741263-A1.

XX
 PD 06-NOV-1997.

XX
 PF 28-APR-1997; 97WO-US07676.

XX
 PR 29-APR-1996; 96US-0640389.

XX
 PA (PROG-) PROGENITOR INC.

PI Clotoff J, Shafer AW, Snodgrass RH, Zupancic TJ;

XX
 DR WPI; 1997-549757/50.

XX
 DR N-PSDB; AAT95781.

XX
 PT Detecting defective obese protein or leptin receptor in reproductive
 XX cells - using variant receptor gene specific probes

XX
 PS Disclosure; Fig 3; 40pp; English.

XX
 CC The present sequence was used in the development of a novel method
 CC for detecting a defective obese protein or leptin receptor (OB-R)
 CC in cells. The method comprises contacting RNA extracted from a
 CC cell population (preferably an ovary, prostate, testis, sperm, ova,
 CC ovarian follicular or blood cell population) with an
 CC oligonucleotide derived from a portion of the human OB-R variant
 CC Form 1, 2 or 3 cDNA, and detecting hybridisation. Forms 2 and 3 are
 CC associated with infertility, as they are unable to correctly
 CC transduce signals from leptin binding. The detection method can be
 CC used to diagnose infertility, or predisposition to infertility,
 CC while treatments that inhibit or down regulate the variants, gene
 CC therapy to replace them in homozygotes or direct activation of
 CC downstream signal transduction can be used to improve fertility.
 CC Also described is the use of labelled DNA probes based on the OB-R
 CC sequence to screen for other variants.

XX
 SQ Sequence 896 AA;

Query Match

99.18; Score 4325; DB 18; Length 896;

Best Local Similarity 99.4%; Pred. No. 0;
 Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MICORFCVLLHWEFYVITAFNLSTYPTPWRFKLSCMPNSTYDYFLPLAGLSKNTS 60
 DB 1 micorfcvllhwefyvitafnlstyptrwrfklscompnstydyflplagsknts 60
 QY 61 NGHYETAVEPKFNSSGTHFSNLSKTFHCCFRSEODRNCISLCAADIEGTFVSTVNSLVF 120
 DB 61 ngyetavepkfnsgthfnsnlskthccfrseodrnscslcadiegtfvstvnslvf 120
 QY 121 QOIDANNIQCWLKGLDLKLFICYVESLKFKNLFRNTNYKVHLLYVLPVELEDSPLVPQKGS 180
 DB 121 qqidanwnlqclwklkdlklyficyveslfnlfrnnykvhllylvpleledsplvpqkgs 180
 QY 181 FQMVHCNSVHECCBCLVPVPTAKLNDLMLCKITSGVIFQSPMSVQPINMYKPPPP 240
 DB 181 fgmvhcnsvheccbclvpvptaklndlmlckitsgvifqspmsvqipnmvkdppp 240
 QY 241 LGLHMEITDDGNLKIWSWSPPLVPFPLOYQVQKYSNSTTVIREADKIVSATSLVDSILP 300
 DB 241 lglhmeitddgnlkiwswwspplvpfploqvqvksnsttvireadkivsatsllvdsilp 300
 QY 301 GSSYEVQVRGKRLDGPISWDMSTPRVFTTQDVIYFPFKILTSVGSNVSFHCYKKNKI 360
 DB 301 gssyevqvrgrldgplswdmsprvfttdqvifypfkiltsvgnsnvsfhiykkenki 360
 QY 361 VPSKEIVWMLAEKIPQSDVDVSDHVSQVTFNLTNPKRGKFTYDAVYCCNEHECHH 420
 DB 361 vpskeivwmlaekipqsdvvdvshvskvtfnltnpkrgkftydavycnehechh 420
 QY 421 RYAEIYVIDVNIINISCEITDGYLTMTKTCRWSTSTQSLAESTLQRLRYHSSLYCSDIPSII 480
 DB 421 ryaeliyvidvniiniscetdgytmtkcrwststqslaelstqlryhsslycsdipsii 480
 QY 481 PISEPKDCYLQSDGFEYECIFQPIFLLSGYTMIRINHSLSGLDSPPTCVLPDSVVKPLPP 540
 DB 481 pisepkdcylqsdgfyecifqipifllsgytmirinhslsgldspptcvlpdsvvkplpp 540
 QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSKEVQWKMVEYDAKSVSULPV 600
 DB 541 ssvkaeitinigllkiswekpvfpennlofqirylskevqwkmyevydaksvsulpv 600
 QY 601 PDLCAVAVQVRCKRLDGLGYWSNWNPNAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
 DB 601 pdlcavavqvrckrlidggywsnwnpnaytvvmdikvpmrgpefwrriingdtmkkeknv 660
 QY 661 TLLWKPLMKNDLSQVQRYVINHTSCNGTWSQEDVGNHTKFTFLWTEQAHVTVLAINSI 720
 DB 661 tllwkpmlkndlsqvrqyvinhtscngtwsedvgnhktftflwteqahvvtvlainsi 720
 QY 721 GASVANFNLTFSWPMKSNVIVQSLASAYPLNSCVIVSWILSPSDYKLMYFIIEWKNLNED 780
 DB 721 gasvanfnltfswpmksnvivqslasayplnscvsvilswilspdyklymfiiewknlnd 780
 QY 781 GEIKWLRISSVKKYYIHGKF 801
 DB 781 geikwlriissvkkyyihdhf 801

RESULT 12

AAW50002
 ID AAW50002 standard; Protein; 904 AA.

XX
 AC AAW50002;

XX
 DT 11-JUN-1998 (first entry)

XX
 DE Human OB-R variant Form 2.

XX
 KW Detection; defective obese protein receptor; defective OB-R; human;
 XX defective leptin receptor; variant Form 2; infertility.

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OS  Homo sapiens.
XX  WO9741263-A1.
XX  PD 06-NOV-1997.
XX  PF 28-APR-1997; 97WO-US07676.
XX  PR 29-APR-1996; 96US-0640389.
XX  PA (PROG-) PROGENITOR INC.
XX  PI Cloffi J, Shafer AW, Snodgrass RH, Zupancic TJ;
XX  DR WPI: 1997-549757/50.
XX  DR N-PSDB; AAT95779.
XX  PT Detecting defective obese protein or leptin receptor in reproductive
XX  cells - using variant receptor gene specific probes
XX  PS Disclosure; Fig 3; 40pp; English.
XX  CC The present sequence was used in the development of a novel method
XX  for detecting a defective obese protein or leptin receptor (OB-R)
XX  in cells. Them method comprises contacting RNA extracted from a
XX  cell population (preferably an ovary, prostate, testis, sperm, ova,
XX  ovarian follicular or blood cell population) with an
XX  oligonucleotide derived from a portion of the human OB-R variant
XX  form 1, 2 or 3 cDNA, and detecting hybridisation. Forms 2 and 3 are
XX  associated with infertility, as they are unable to correctly
XX  transduce signals from leptin binding. The detection method can be
XX  used to diagnose infertility, or predisposition to infertility,
XX  while treatments that inhibit or down regulate the variants, gene
XX  therapy to replace them in homozygotes or direct activation of
XX  downstream signal transduction can be used to improve fertility.
XX  Also described is the use of labelled DNA probes based on the OB-R
XX  sequence to screen for other variants.
XX  SQ Sequence 904 AA;

Query Match 99.1%; Score 4325; DB 18; Length 904;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MICOKFCVLLHWEFIVYAFNLSDYTPWRKFLSCMPNPNSTVDYFLLPAGLSKNTS 60
DB 1 micqkfcvllhwefiyvitafalsytpwrkflscmpnpnstydyfllpaglsknts 60
QY 61 NGHYETAPEKFNSSGTHFNLKSTTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
DB 61 nghyetapekfnsngthfnlsksttfhccfrseodrnscslcadniegrtfvstvnslvf 120
QY 121 QQIDANNIOCLKGLDLKICVESLFKFLNRYNKHLLVLPVLEDSPLVPQKGS 180
DB 121 qqidanwncwlgkldlkciveslfkflnrynkhllylvpvlecdslvpqkgs 180
QY 181 FQWVHCNCSVHECECLVPVPTAKLNDTLMLKIRSGGVIFOSPLMSVOPINNKVPDPP 240
DB 181 fqmwhncsvhececlvpvptaklndtlmlckitrgsggvifrsplmsvqpinmvpdpdp 240
QY 241 LGLHMETDGNLKIWSPPPLFPLOQYKYSNSTVIREADKIVSATSLVDSILP 300
DB 241 lglhmeitdgnlkiwsppplfploqykysnstvireadkivsatsllvdsilp 300
QY 301 GSSYEYQVRKRLDGPICWSDWSTPRVFTTODVIYPPPKLTTSVGSNVSFHCYKKNKI 360
DB 301 gssyeqvqrkrlldgpgicwswdwtprvfttdviiypppklttsvgnsfphciykkenki 360
QY 361 VPSKEIWMNLAEPQSQDYDVSVSHSVKTFPFLNETKPRGKFTYDAVYCCNEHECHH 420
DB 361 vpskeiwmnlaekipqsgdydvsvshsvkvtfflnetkprgkftdyavycnehechh 420

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421 RYAEIYVIDVINISCEPDTGYLTKMTCRWSTSTIOSLAESTLQIRYHRSSLYCSDIPSIIH 480
 DB RYAEIYVIDVINISCEPDTGYLTKMTCRWSTSTIQSLAESTLQIRYHRSSLYCSDIPSIIH 480
 QY PISEPKDCYLOSDFEYECIFOPIFLLSGYTMWIRINHSLGSLDPTCVLPDSVVKPLPP 540
 DB PISEPKDCYLOSDFEYECIFOPIFLLSGYTMWIRINHSLGSLDPTCVLPDSVVKPLPP 540
 QY SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
 DB SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
 QY PDLCAVAVQVRCKRLDGLGYWNSNPNPAYTVVMDIKVPMRGPEFWIRINGDTMKKKNV 660
 DB PDLCAVAVQVRCKRLDGLGYWNSNPNPAYTVVMDIKVPMRGPEFWIRINGDTMKKKNV 660
 QY TLLWPKMLKNDLSGVORYVINHHTSCNGTWSEVGNHKTETFLWTOAHVTVLAINSI 720
 DB TLLWPKMLKNDLSGVORYVINHHTSCNGTWSEVGNHKTETFLWTOAHVTVLAINSI 720
 QY GASVANFNLTSPWMSKVINIYQSLAYSPLNSSCVIVSWILSPSDYKLMFYFIENKLNED 780
 DB GASVANFNLTSPWMSKVINIYQSLAYSPLNSSCVIVSWILSPSDYKLMFYFIENKLNED 780
 QY GEIKWLRISSVKKYIYHGRF 801
 DB GEIKWLRISSVKKYIYHGRF 801
 RESULT 13
 AAW38214
 ID AAW38214 standard; Protein; 958 AA.
 AC AAW38214;
 XX 11-JUN-1998 (first entry)
 DT Human OB-R variant Form 1.
 DE Detection: defective obese protein receptor; defective OB-R; human;
 KW defective leptin receptor; variant Form 1; infertility.
 OS Homo sapiens.
 XX WO9741263-A1.
 XX 06-NOV-1997.
 XX 28-APR-1997; 97WO-US07676.
 XX 29-APR-1996; 96US-0640389.
 XX (PROG-) PROGENITOR INC.
 XX Cloffi J, Shafer AW, Snodgrass RH, Zupancic TJ;
 XX WPI: 1997-549757/50.
 XX N-PSDB; AAT95779.
 XX Detecting defective obese protein or leptin receptor in reproductive
 XX cells - using variant receptor gene specific probes
 XX Disclosure; Fig 3; 40pp; English.
 XX The present sequence was used in the development of a novel method
 XX for detecting a defective obese protein or leptin receptor (OB-R)
 XX in cells. Them method comprises contacting RNA extracted from a
 XX cell population (preferably an ovary, prostate, testis, sperm, ova,
 XX ovarian follicular or blood cell population) with an
 XX oligonucleotide derived from a portion of the human OB-R variant
 XX form 1, 2 or 3 cDNA, and detecting hybridisation. Forms 2 and 3 are
 XX associated with infertility, as they are unable to correctly
 XX transduce signals from leptin binding. The detection method can be
 XX used to diagnose infertility, or predisposition to infertility,
 XX while treatments that inhibit or down regulate the variants, gene
 XX therapy to replace them in homozygotes or direct activation of
 XX downstream signal transduction can be used to improve fertility.
 XX Also described is the use of labelled DNA probes based on the OB-R
 XX sequence to screen for other variants.

CC used to diagnose infertility, or predisposition to infertility,
CC while treatments that inhibit or down regulate the variants, gene
CC therapy to replace them in homozygotes or direct activation of
CC downstream signal transduction can be used to improve fertility.
CC Also described is the use of labelled DNA probes based on the OB-R
CC sequence to screen for other variants.
XX
SQ Sequence 958 AA;

Query Match 99.1%; Score 4325; DB 18; Length 958;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIVYVTAFLNLPYIPWFKLSKMPNPNSTYDYFLPAGLSKNTNS 60
Db 1 micqkfcvllhwevlyvtafnlspypwfklskmpnnpnstydyflpagskntns 60
QY 61 NGHYETAVPEKFNSSOTHTFNSKTTFFHCCFSEQRNCSLACADNIEGRTFVSTVNSLVF 120
Db 61 nghyetavpekfnssgthfnskttffhccfseqrncslcadniegrtfvstvnslvf 120
QY 121 QOIDANNITQCLKGLKLFICVSELSFKNLFRNYKVVHLLVYLPVLEDSPLVPQKGS 180
Db 121 qoidannitqclkgldkflfcvselsfknlfirnykvvhllvylpveledsplvpqkgs 180
QY 181 FQMVHCNCSVHECCCLVPVPTAKLMDTLMLCKITSGVIFQSPMSVQPINMVKPDP 240
Db 181 fqmvhcnscsvheccclvpvptaklmdtlmlckitsgvifrspmsvqipnmvkpdp 240
QY 241 LGLHWEITDGNLKTSSWSPPLVPPLQVQVYSENSTTVIREADKIVSATSLLVDSILP 300
Db 241 lglhmeitdgnlktsswspplvpplqvqvysensttvireadkivsatsllvdsilp 300
QY 301 GSSYEYQVRGKRLDGGIWSNSTPRVFTQDVIVFPFKILTSGVSNYSFHCYKKNKI 360
Db 301 gssyeqvrgkrlldgglwstprvftqdvivfppkiltsgvsnysfchcykknki 360
QY 361 VPSKEIVWMNLAEKIPQSQYQVSDVSHSVKVTFFNLNETKPRGFTYDAVYCCNEHECHH 420
Db 361 vpskeivwmnlaeqipqsqyvsvdshsvkvtffnlnetkprgftdyavycnehechh 420
QY 421 RYAEIYVIDVNIINISCTDGYITKTCRWSTSTIOSLAESTQLQRYHRSLSYCSIPSIH 480
Db 421 ryaeliyvidvniiniscetdgyitktrcwststioslaestqlqlyhrsslycsdipsh 480
QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGVTMIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
Db 481 pisepkdcylsdgfyecifqpfifllsgvtymirinhslgsldspptcypdsvvkplpp 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLPQFQIRYGLSGKEVQWKNYEVYDAKSVSPLV 600
Db 541 ssvkaeitinigllkiswekpvfpennlpqfiryglsgkevqwnyevydaksvsplv 600
QY 601 PDLCAVYAVQVCKRLDGLGYSWNSNAYVVMVDKIPMRGPETWRINGDTMKKERNV 660
Db 601 pdlcavayavqckrldglgyswnsnayvvmvdkipmrpgetwringdtmkkernv 660
QY 661 TLWKPLMKNDLSQVQRVIVNHHTSCNWTSEEDVGNHTKFTFLWTEQARTVTVLAINSI 720
Db 661 tlwkpmlkndlsqvrivnhhtscnwtseedvgnhtkftflwteqartvtvvlainSI 720
QY 721 GASVANFNLTSWPMKSNVIVQSLSAYPLNSCVIVSWILSPSDYKLMFYIEMKNLNE 780
Db 721 gasvanfntltswpmksnvivqslsayplnscvsvilspdyklnfyiemknlne 780
QY 781 GEIKWLRISSSVKKYIIGKFP 801
Db 781 geikwlrisssvkkyyihdhf 801

RESULT 14
AAW31911

ID AAW31911 standard; Protein; 958 AA.
XX
AC AAW31911;
XX
DT 02-FEB-1998 (first entry)
XX
DE Human OB-R leptin receptor variant.
XX
KW Leptin receptor; OB-R; obese gene; obesity; gene therapy;
diagnosis; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 85 /note= "variation from published sequence"
FT Misc-difference 109 /note= "variation from published sequence"
FT Misc-difference 223 /note= "variation from published sequence"
FT Domain 845..862 /label= Transmembrane_domain
FT Misc-difference 892..958 /note= "divergence from published sequence"
XX
PN W09726370-A1.
XX
PD 24-JUL-1997.
XX
PF 17-JAN-1997; 97WO-US00570.
XX
PR 18-JAN-1996; 96US-0508190.
XX
PA (PROG-) PROGENITOR INC.
XX
PI Cioffi J, Shafer AW, Snodgrass HR, Zupancic TJ;
DR WPI; 1997-385353/35.
XX N-PSDB; AAT89193.
PT Detecting defective leptin receptor by hybridisation assay - and
PT treatment of obesity with agent that inhibits the defective
PT receptor, also screening for compounds that supplement leptin
PT activity
XX
PS Claim 12; Fig 1A-E; 26pp; English.
XX
CC This polypeptide comprises a variant of the human leptin receptor
CC (OB-R). Its sequence was deduced from a contiguous cDNA (AAT89193)
CC derived from overlapping clones isolated from a human foetal liver
CC library. The sequence shows near identity to a published OB-R
CC sequence in the extracellular domain, with the exception of 3 amino
CC acids, but there is extensive diversity in the intracellular
CC cytoplasmic domain at the C-terminal end. A claimed method for
CC detection of OB-R in cells comprises extraction of RNA and testing
CC this for hybridisation to an oligonucleotide (I) derived from the
CC OB-R variant gene, especially from the region beyond nucleotide
CC 2770. Also claimed are methods of: (1) treating obesity by
CC administration of an agent that inhibits expression of the OB-R
CC variant gene; and (2) identification of a compound that can
CC supplement activity of leptin by: (i) incubating cells expressing
CC OB-R variant first with leptin and then with a test compound, and
CC (ii) comparing activation signals between cells treated and not
CC treated with the test compound. Inhibition/down-regulation of the
CC variant OB-R (found in obese people) improves response of cells to
CC weight regulation by leptin. Replacing variant OB-R by gene therapy
CC (in homozygous individuals) can be used to treat obesity. Labelled
CC probes based on the gene can be used to isolate other variant forms
CC of the receptor gene or to detect the variant gene (e.g. for
CC determining predisposition to obesity), while the OB-R gene can be
CC used to express recombinant OB-R (optionally as fusion protein) and
CC in standard hybridisation assays. The OB-R gene can also be used
CC therapeutically in cases of overexpression of functional OB-R

CC (causing loss of appetite and hypermetabolic activity). Cells
 CC engineered to express variant receptor are used in method (2) to
 CC screen for (ant)agonists of leptin/OB-R interaction, also to generate
 CC antibodies that competitively inhibit, neutralise or enhance activity
 CC of the variant receptor.
 XX
 SQ Sequence 958 AA;

Query Match 99.1%; Score 4325; DB 18; Length 958;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIVYVTAFLNLSPTIPWRKLSKMPNPNSTYDFLLPAGLSKNTS 60
 DB 1 micqkfcvllhwevlyvatfnlsyptipwrfklsmpnpsndydfllpaglskntsn 60
 QY 61 NGHYETAPEKFNSTHFSNLSKTTFHCCFSEQRNCSLCADNTEGKTFVSTVNSLVF 120
 DB 61 nghyetapekfnsghfshnskathccfseqrncslcadnlegtfvstvnslvf 120
 QY 121 QQIDANNTQCKLKGDKLFCYVESLFKFLFNRYKVLHLLVLEPVEDSLVPQKGS 180
 DB 121 qqidanwnlqcklkgdklfcyveslfkflfnrykvhllylvpvledslvpqkgs 180
 QY 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGGVIFQSPMLSVOPINMVKPDP 240
 DB 181 fgmvhcnscsvheccclvpvptaklndtlmlckitsggvifrsplmsvqpinmvpkdp 240
 QY 241 LGLHMEITDGNLTKISWSSPPLVPPLOXQVYSESTTVIREADKIVSATSLLVDSILP 300
 DB 241 lglhmeitdgnltkiswsspplvpplqxvysensttvireadkivsatsllvdsilp 300
 QY 301 GSSYEVQVRKRLDGFSGIWSMSTPRVFTQDVIYPPPKILTSVGSNVSFHCYIKKENKI 360
 DB 301 gssyevqvrkrlgpgglwsdstprvftqdvlyfppkiltsgvsnvsfchcyikkenki 360
 QY 361 VPSKEIVWNNLAERIPQSDYDWDHVSQVTFNNLNETKPRGKFTYDAVYCCNHECHH 420
 DB 361 vpskeivwvnnlaekipqsgdydwdhvsqvtfnlnetkprgkftdyavycnechhh 420
 QY 421 RYAEIYVIDVNIISCTDGYLTMTCKRWSTIQSLAESTLQLRVHRSLSYCSIDPSTH 480
 DB 421 ryaelyvdiwniisctdgyltmckrwtstiqslaestlqlrvhrsslycsidpsih 480
 QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMMIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
 DB 481 pisepkdcylqsdgfyecifqpfllsgytmwirinhslgslidspptcylpdsvvpkplpp 540
 QY 541 SSVKAEITINIGLLKISWKPFPENNLQFQIRYGLSGKEVQWKYEVYDAKSKSVSLPV 600
 DB 541 ssvkaeitinigllklswekpfpennlqfiryglsgkevqwkmyevydaaksksvslpv 600
 QY 601 PDLCAVYAVQVRCKRLDGLGYSNNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKV 660
 DB 601 pdlcavayavvrckrldglgywnsnnpaytvvmdikvpmrgpewriingdtmkkeknv 660
 QY 661 TLWLKPLMKNDSCSVQRVIVINHHTSCNWTSEDVGNHTKFTFLTEQAHVTVLAINSI 720
 DB 661 tlwlkplmkndscsvqrvivnhhtscngtwsedvgnhtkftflteqahvtvvlainsi 720
 QY 721 GASVANFNITFSWPMKVNIVOSLSAYPLNSSCVISWTLSPSDYKLMYFIIEKNLNEB 780
 DB 721 gasvanfnitfswpmkvnivoslaysayplnsscvilswtllpsdyklyfiieknlned 780
 QY 781 GEIKLRLIRSSSVKKYIHKPF 801
 DB 781 geiklrlirsssvkkyihdhf 801

RESULT 15

AAW19535

ID AAW19535 standard; Protein; 958 AA.

XX AAW19535;
 XX 02-FEB-1998 (first entry)
 DT Human OB-R leptin receptor variant.
 DE
 XX
 KW Leptin receptor; OB-R; obese gene; obesity; gene therapy;
 KW diagnosis; human.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 85
 FT /note= "variation from published sequence"
 FT Misc-difference 109
 FT /note= "variation from published sequence"
 FT Misc-difference 223
 FT /note= "variation from published sequence"
 FT /note= 845..862
 FT Domain /label= Transmembrane_domain
 FT Misc-difference 892..958
 FT /note= "divergence from published sequence"
 XX WO9726272-A1.
 PN
 XX
 XX 24-JUL-1997.
 PD
 XX
 PF 17-JAN-1997; 97WO-US00880.
 XX
 PR 18-JAN-1996; 96US-0588189.
 XX
 PA (PROG-) PROGENITOR INC.
 XX
 PI Cioffi J, Shafer AW, Snodgrass HR, Zupancic TJ;
 XX WPI: 1997-385291/35.
 DR P-PSDB; AAT72649.
 XX
 PT - With oligonucleotide derived from DNA of receptor variant RNA
 PT - detecting defective form of leptin receptor by probing cellular RNA
 PT - treatment of obesity by inhibiting expression of variant receptor
 PT - and screening for agents that increase leptin activity
 XX Claim 12; Fig 1A-E; 26pp; English.

XX This polypeptide comprises a variant of the human leptin receptor
 CC (OB-R). Its sequence was deduced from a contiguous cDNA (AA72649)
 CC derived from overlapping clones isolated from a human foetal liver
 CC library. The sequence shows near identity to a published OB-R
 CC sequence in the extracellular domain, with the exception of 3 amino
 CC acids, but there is extensive diversity in the intracellular
 CC cytoplasmic domain at the C-terminal end, suggesting alternative
 CC splicing of a common precursor mRNA. A claimed method for
 CC detection of OB-R in cells comprises extraction of RNA and testing
 CC this for hybridisation to an oligonucleotide (I) derived from the
 CC OB-R variant gene, especially from the region beyond nucleotide
 CC 2770. Also claimed are methods of: (1) treating obesity by
 CC administration of an agent that inhibits expression of the OB-R
 CC variant gene; and (2) identification of a compound that can
 CC supplement activity of leptin by: (i) incubating cells expressing
 CC OB-R variant first with leptin and then with a test compound, and
 CC (ii) comparing activation signals between cells treated and not
 CC treated with the test compound. Inhibition/down-regulation of the
 CC variant OB-R (found in obese people) improves response of cells to
 CC weight regulation by leptin. Replacing variant OB-R by gene therapy
 CC (in homozygous individuals) can be used to treat obesity. Labelled
 CC probes based on the gene can be used to isolate other variant forms
 CC of the receptor gene or to detect the variant gene (e.g. for
 CC determining predisposition to obesity), while the OB-R gene can be
 CC used to express recombinant OB-R (optionally as fusion protein) and
 CC in standard hybridisation assays. The OB-R gene can also be used
 CC therapeutically in cases of overexpression of functional OB-R

CC (causing loss of appetite and hypermetabolic activity). Cells
CC engineered to express variant receptor are used in method (2) to
CC screen for (ant)agonists of leptin/OB-R interaction, also to generate
CC antibodies that competitively inhibit, neutralise or enhance activity
CC of the variant receptor.
XX
SQ

Sequence 958 AA;

Query Match	99.1%;	Score 4325;	DB 18;	Length 958;
Best Local Similarity	99.4%;	Pred. No. 0;		
Matches 796;	Conservative 2;	Mismatches 3;	Indels 0;	Gaps 0;
QY	1	MICQKFCVLLHWEFIYVITAFNLSPITPPRFKLSCLMPPNSTYDYFLLPAGLSKNTSNS	60	
Db	1	micqkfcvllhwefiyvitafnlspitpprfklsclmppnstydyfllpagskatsns	60	
QY	61	NGHYETAVPEKFNSSGTHFSNLSKTFHCCEFRSEQRNCSLCAADNIEGRTFVSTVNSLVF	120	
Db	61	nghyetavepkfnssgthfnsksatfhccfrseqdrncslcadniegrtfvstvnslvf	120	
QY	121	QOIDANWNIQCHLKGDLKLFICYVESLKFNLFRNYYKVHLLYVLPVLEDSPLYVQKGS	180	
Db	121	qqidanwnlqcvlkgdlklficyveslfnlfrnynkvhllvlpvledsplyvpqkgs	180	
QY	181	FQVHCNCSVHECCCLVPVPTAKLNDTLMLCLTKTSGVIFQSPLSVQPINNVKPDPP	240	
Db	181	fqvhcnscsvheccclvpvptaklndtlmlcltkitsgvifrspmsvqpinmvkpdpp	240	
QY	241	LGLHMEITDDGNLKTSSPPLVPPPLQYQVYKYSNSTTVIREADKIVSATSLLVDSILP	300	
Db	241	lgllhmeitddgnlktsspplpvpfpqyqykysensttvireadkivsatsllvdsilp	300	
QY	301	GSSYEVQVRGRKLDGPGIWSQSWSTPRVFTTQDVIFPPPKILTSVGSNNVSFHCYKKNKI	360	
Db	301	gssyevqvrgrldgpgiwsdswstprvfttdqvifppkiltsvgsnvsfhiyknkni	360	
QY	361	VPSKEIYVMMNLAEKIPQSQYDVVDVSHVSKVTFFNLNETKPRGFTYDVAVCCNEHCHH	420	
Db	361	vpskeiyvwmnlaeqipsgydvvdshvskvtfnlnetkprgftdydavyccnehechh	420	
QY	421	RYAELYVIDVNNINISCTDGYLTMTKRWSTSTIOSLAESTLQRYHRSSLYCSDIPSIIH	480	
Db	421	ryaelyvldvnninisctdgyltkmtcrwststioslaestlqryhrsslycsdipsih	480	
QY	481	PISBPKCQYLQSDGFYECIFQPIELLSGYTMMIRINHSLSGLSDSPPTCVLPDSVVKPLPP	540	
Db	481	pisbpkcyqsdgfyecifqipifllsgytmwirinhslgslsdspptcvlpdsvvkplpp	540	
QY	541	SSVKAETIINIGLLKISWEKVPFPENNLFQIRYGLSGKEVQWKMEYEVYBAKSKSVSLPV	600	
Db	541	ssvkaetiniigllkiswekvpfpennlfqiryglsgkevqwkmyevybaksksvslpv	600	
QY	601	PDLCVAVQVRKRLDGLGYSWNSNPATVYVMDIKVPMRGPPEFNRINGDTMKKEKNV	660	
Db	601	pdlcavayvrckrldglgyswnsnpatyvmdikvpmrgpfevnrilingdtmkkeknv	660	
QY	661	TLWKPLMKNDLSLCSQVRYVINHHTSCNGTWSQEDVGNHTKFTFLWTEQAHTVTVLAINSI	720	
Db	661	tlwkpmlkndslcsqvyvinhhtscngtwsedvgnhtkftflwteqahtvtvlainsl	720	
QY	721	GASVANFNLTFSWPMKSNIVNQSLSAVPLNNSCVIVSWILSPSDYKLMVPIIEWKNLNE	780	
Db	721	gasvanfnltfswpmksnivnqslsavplnnsccvivswilspdyklmvpfiiewknlne	780	
QY	781	GEIKWLRISSSVKKYYIHGKF 801		
Db	781	geikwlrissvkkyyihdhf 801		

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OM protein - protein search, using sw model

Run on: October 22, 2001, 16:03:50 ; Search time 21.72 Seconds
(without alignments)
2819.721 Million cell updates/sec

Title: US-09-116-676-10

Perfect score: 4363

Sequence: 1 MICQKFCVLLHWEFIYVIT.....WLRISVVKKYYIHGKETIL 804

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*
1: Pirl.*
2: Pirl.*
3: Pirl.*
4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3355	76.9	805	2 S68441	leptin receptor, s
2	3345	76.7	892	2 S68439	leptin receptor, s
3	3345	76.7	894	2 S68437	leptin receptor, s
4	3345	76.7	900	2 S68440	leptin receptor, s
5	3345	76.7	1162	2 S68438	leptin receptor, s
6	3342	76.6	1162	2 PC4184	leptin receptor, O
7	3284	75.3	895	2 S74225	leptin receptor, i
8	296	6.8	917	2 I49699	glycoprotein 130 -
9	277.5	6.4	918	2 A36337	membrane glycoprot
10	270.5	6.2	918	2 A44257	interleukin-6 sign
11	246.5	5.6	837	2 A34898	granulocyte colony
12	242.5	5.6	771	2 B38252	granulocyte colony
13	242.5	5.6	783	2 JH0329	granulocyte colony
14	242.5	5.6	863	2 C38252	granulocyte colony
15	221.5	5.1	1097	2 S17308	leukemia inhibitor
16	220	5.0	2302	2 T14328	protein-tyrosine-p
17	208	4.8	1092	2 JX0312	differentiation-st
18	178	4.1	831	2 JQ1655	prolactin receptor
19	166.5	3.8	2029	1 TDFFLK	protein-tyrosine-p
20	165	3.8	630	2 I51086	prolactin receptor
21	163	3.7	6805	2 S20901	titin - rabbit (fr
22	161.5	3.7	26926	1 I38344	titin, cardiac mus
23	157	3.6	830	2 I50455	prolactin receptor
24	157	3.6	1375	2 T13822	frazzled gene prot
25	153.5	3.5	440	2 JI0144	interleukin-6 rece
26	153.5	3.5	460	2 JI0145	interleukin-6 rece
27	150.5	3.4	3210	2 A29884	prolactin receptor
28	150.5	3.4	412	2 A41070	prolactin receptor
29	150.5	3.4	610	2 A36116	prolactin receptor

30 149.5 3.4 1197 2 T30581
31 149 3.4 3488 2 T34418
32 148 3.4 1000 2 I46521
33 148 3.4 1526 2 T13823
34 147.5 3.4 610 2 A34631
35 147.5 3.4 1232 2 T43027
36 146 3.3 2338 2 I73957
37 144 3.3 1825 2 T32828
38 143 3.3 638 2 A33991
39 142 3.3 1447 2 A54100
40 141 3.2 581 2 I45971
41 141 3.2 878 1 A40091
42 140.5 3.2 638 2 B28176
43 140.5 3.2 638 2 S12136
44 139 3.2 579 2 B45266
45 139 3.2 635 2 A45266

ALIGNMENTS

RESULT 1

S68441 leptin receptor, splice form Ob-Re - mouse

C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-2000 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000

C:Accession: S68441

R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; Nature 379, 632-635, 1996

A:Title: Abnormal splicing of the leptin receptor in diabetic mice.

A:Reference number: S68437; MUID:96231997

A:Accession: S68441

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 1-805 <LE>

A:Cross-references: EMBL:U49110; NID:gl195492; PIDN:AAC52424.1; PID:gl1195493

A:Experimental source: splice form Re; tissue hypothalamus

A:Note: The nucleotide sequence was submitted to the EMBL Data Library, February 1996

C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:

C:Genetics:

A:Gene: Ob-Re

C:Keywords: alternative splicing; appetite

Query Match 76.9%; Score 3355; DB 2; Length 805;
Best Local Similarity 76.0%; Pred. No. 5,3e-227;
Matches 611; Conservative 74; Mismatches 117; Indels 2; Gaps 2;
QY 1 MICQKFCVLLHWEFIYVITAFNLSPYTPMRFKLSCMPNSTYDYFLPLAGLSKNTNS 60
DB 1 MMCQKFCVLLHWEFIYVITAFNLSPYTPMRFKLSCMPNSTYDYFLPLAGLSKNTNS 60
QY 61 NCHYETAPEPFNSGTHFNSLSKTTFFHCCPRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
DB 61 KGASAIPEAFNSGTHFNSLSKTTFFHCCPRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QOIDANNIQCWLKGLKFLCYVBSLFKNLFRNRYKHLVLYLVELEDSPLVPQKGS 180
DB 121 ROLGVNWDIECMKGLDLFLFCHMEPLKPNFKNDKSVHLLYDLPEVIDDSPLPLKDS 180
QY 181 FQVHCNCSVHCCBCLVPVPTAKLNDTLMLCKITSGVIFQSPMSVQPIVMYKPPPP 240
DB 181 FQVHCNCSVHCCBCLVPVPTAKLNDTLMLCKITSGVIFQSPMSVQPIVMYKPPPP 240
QY 241 LGLHMEITDDGNLKSWSPPPLPQYQYKNSNTVIREADKIVSATSLLVDSILP 300
DB 241 LGLHMEITDDGNLKSWSPPPLPQYQYKNSNTVIREADKIVSATSLLVDSILP 300
QY 301 GSSYEVQVRGRKLDGPGIWSDMSTPRVFTTODVYFPFKILTSGVSNVSFHCYKKNKI 360
DB 301 GSSYEVQVRGRKLDGPGIWSDMSTPRVFTTODVYFPFKILTSGVSNVSFHCYKKNKI 360
QY 361 VPSKEIVWMNLAEKIPQSDYDVVSDHVSQVTFNMLNETKPRGKFTYDAVYCCNEHCCH 420

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Db 359 ISSKQIVWMRLAEKIPKQSIYSDRVSKVTFNSLKAIRGRFTYDAVYCCNEQACHH 418
QY 421 RYAEYLVIVDNNINISCEFDGVLTKTCTCRWSTSTQSLAESTLQRLYRHSLSYCDIPSIIH 480
Db 419 RYAEYLVIVDNNINISCEFDGVLTKTCTCRWSTSTQSLVGSVQLRYRHSLSYCDPSIIH 478
QY 481 PISEPKDCYVQSDGFEICFQIFELLGSGYVWIRINISLGSLSDDSPPTCVLPDSVVKPLPP 540
Db 479 PISEPKDCYVQSDGFEICFQIFELLGSGYVWIRINISLGSLSDDSPPTCVLPDSVVKPLPP 538
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMVEYVDAKSKSVSLPV 600
Db 539 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMVEYVDAKSKSVSLPV 598
QY 601 PDLCAVAVOVRCKRLDGLGYSWNSNPAYTVVMDIKVPMRGPEFWRIRINGDTPMKKEKNV 660
Db 599 PDLCAVAVOVRCKRLDGLGYSWNSNPAYTVVMDIKVPMRGPEFWRIRINGDTPMKKEKNV 658
QY 661 TLLWPKMLKNDLSLCSVQRYVYINHTSCNGTWSVDGNGHTKFTFLWTEQAHVTVLAINSI 720
Db 659 TLLWPKMLKNDLSLCSVQRYVYINHTSCNGTWSVDGNGHTKFTFLWTEQAHVTVLAINSI 718
QY 721 GASVANFNLTFSWPMKSVNIVQSLAYSPLNSCVIVSWILSPSDYKLMYFIIEWKNLNED 780
Db 719 GASVANFNLTFSWPMKSVNIVQSLAYSPLNSCVIVSWILSPSDYKLMYFIIEWKNLNED 778
QY 781 GEIKWLRISSSVKYYIHGKFTLL 804
Db 779 DGMKWLRIPSNVKAFYIHDNF 802

RESULT 2
S68439
leptin receptor, splice form Ob-Rc - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-2000 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000
C:Accession: S68439; S68441
R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; F
Nature 379, 632-635, 1996
A:Title: Abnormal splicing of the leptin receptor in diabetic mice.
A:Reference number: S68437; MUID:96231997
A:Accession: S68439
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 664-892 <LEE1>
A:Cross-references: EMBL:U49110; NID:g1195492; PIDN:AAC52424.1; PID:g1195493
A:Experimental source: splice form Rc; tissue hypothalamus
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C:Comment: For alternative splice form Re is included to produce a complete sequence
C:Genetics:
A:Gene: Ob-Rc
C:Keywords: alternative splicing; appetite

Query Match 76.7%; Score 3345; DB 2; Length 892;
Best Local Similarity 76.0%; Pred. No. 3e-226;
Matches 609; Conservative 73; Mismatches 117; Indels 2; Gaps 2;
QY 1 MICOFCVLLHNEFYIVTAFNLSYPTIPWRKLSGMPNPNYDFLLPAGLSKNTNS 60
Db 1 MICOFCVLLHNEFYIVTAFNLSYPTIPWRKLSGMPNPNYDFLLPAGLSKNTNS 60
QY 61 NGHYETAPEKFNSSGTHSNKTTTHCCFSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
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Db 61 KGASEAIVAEKFNSSGIYVPELSKTVFHCFCGNEQONCSALTDNTEGKTLASVVKASVF 120
QY 121 QOIDDANNICOWLKGDLKLFICYVESLFLKMLFRNYKVKHLLYVLPVELEDSPLVPQKGS 180
Db 121 RQGVNWDIECWMKGDJTLFICHMEPLPKNPKFNKDYKSHLLYDLPEVIDSDPLPLPKDS 180
QY 181 FQVHNCVSHECECECLVPVPTAKLNDTLMLCKLITSGGVIFQSPMLSVQPINVKRPDPP 240
Db 181 FQVHNCVSHECECECLVPVPTAKLNDTLMLCKLITSGGVIFQSPMLSVQPINVKRPDPP 239
QY 241 LGHMEITDGNLKIISWSPPLVPFPLOQVQKYSSENSTTVIREADKIVSATSLVDSILP 300
Db 240 LGHMEITDGNLKIISWSPPLVPFPLOQVQKYSSENSTTVIREADKIVSATSLVDSILP 298
QY 301 GSSYEYQVQVRCKRLDGLGYSWNSNPAYTVVMDIKVPMRGPEFWRIRINGDTPMKKEKNV 360
Db 299 GSSYEYQVQVRCKRLDGLGYSWNSNPAYTVVMDIKVPMRGPEFWRIRINGDTPMKKEKNV 358
QY 361 VPSKEIVWMNLAEKIPQSDYDVYSDHVSQVTFNNELNETKPRGKFTYDAVYCCNEQACHH 420
Db 359 VPSKEIVWMNLAEKIPQSDYDVYSDHVSQVTFNNELNETKPRGKFTYDAVYCCNEQACHH 418
QY 421 RYAEYLVIVDNNINISCEFDGVLTKTCTCRWSTSTQSLAESTLQRLYRHSLSYCDIPSIIH 480
Db 419 RYAEYLVIVDNNINISCEFDGVLTKTCTCRWSTSTQSLVGSVQLRYRHSLSYCDPSIIH 478
QY 481 PISEPKDCYVQSDGFEICFQIFELLGSGYVWIRINISLGSLSDDSPPTCVLPDSVVKPLPP 540
Db 479 PISEPKDCYVQSDGFEICFQIFELLGSGYVWIRINISLGSLSDDSPPTCVLPDSVVKPLPP 538
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMVEYVDAKSKSVSLPV 600
Db 539 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMVEYVDAKSKSVSLPV 598
QY 601 PDLCAVAVOVRCKRLDGLGYSWNSNPAYTVVMDIKVPMRGPEFWRIRINGDTPMKKEKNV 660
Db 599 PDLCAVAVOVRCKRLDGLGYSWNSNPAYTVVMDIKVPMRGPEFWRIRINGDTPMKKEKNV 658
QY 661 TLLWPKMLKNDLSLCSVQRYVYINHTSCNGTWSVDGNGHTKFTFLWTEQAHVTVLAINSI 720
Db 659 TLLWPKMLKNDLSLCSVQRYVYINHTSCNGTWSVDGNGHTKFTFLWTEQAHVTVLAINSI 718
QY 721 GASVANFNLTFSWPMKSVNIVQSLAYSPLNSCVIVSWILSPSDYKLMYFIIEWKNLNED 780
Db 719 GASVANFNLTFSWPMKSVNIVQSLAYSPLNSCVIVSWILSPSDYKLMYFIIEWKNLNED 778
QY 781 GEIKWLRISSSVKYYIHGKFTLL 801
Db 779 DGMKWLRIPSNVKAFYIHDNF 799

RESULT 3
S68437
leptin receptor, splice form Ob-Ra - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-2000 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000
C:Accession: S68437
R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;
Nature 379, 632-635, 1996
A:Title: Abnormal splicing of the leptin receptor in diabetic mice.
A:Reference number: S68437; MUID:96231997
A:Accession: S68437
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-894 <LEE>
A:Cross-references: EMBL:U49106; NID:g1195484; PIDN:AAC52420.1; PID:g1195485
A:Experimental source: splice form Ra; tissue hypothalamus
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:
C:Genetics:
A:Gene: Ob-Ra
C:Keywords: alternative splicing; appetite
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Query Match 76.7%; Score 3345; DB 2; Length 894;
Best Local Similarity 76.0%; Pred. No. 3.le-226;
Matches 609; Conservative 73; Mismatches 117; Indels 2; Gaps 2;

QY 1 MICQFCVLLHWEFIYVITAFNLSYPTTPWRKFLSCMPNNTSYDYFLLPAGLSKNTSNS 60
DB 1 MMCQKFYVLLHWEFLYIAALNLAISPWKFLFCGPPNTDDSFSLPAGAPNNSAL 60

QY 61 NGHYETAPEKFNSSGTHFNLSKTFHCCFRSBDNRCSLCAONIEGKTFVTSVLSVF 120
DB 61 KGASEAIVEAKFNSSGIYVPELSKTFVHCCFNGQNGCSALTONTGKTLASVVKASVF 120

QY 121 QOIDANNIOCLKGLDKLFICYVESLFKNLFNRYNKKVHLLYVLPVLEDSPLVPKGS 180
DB 121 ROLGVNWDIECMKMGDLTLFICHMEPLKPNFKNYDSKVHLLYDLPVIDDSPLPLKDS 180

QY 181 FQVHCNSVHECCLECLVPVPTAKLNDTLMLCKLITSGVTFQSPMLSVQPINVKPDP 240
DB 181 FQVHCNSVHECCLECLVPVPTAKLNDTLMLCKLITSGVTFQSPMLSVQPINVKPDP 240

QY 241 LGLHMEITDDGNLKSWSPPPLVFPFLOQYQVYKYSNSTVIREADKIVSATSLLVDSILP 300
DB 241 LGLHMEITDDGNLKSWSPPPLVFPFLOQYQVYKYSNSTVIREADKIVSATSLLVDSILP 300

QY 301 GSSYEVOVRKRLDGLGYSVNSWSPATVYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
DB 301 GSSYEVOVRKRLDGLGYSVNSWSPATVYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660

QY 661 TLLWKPLMKNDLSVQRYVINIHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI 720
DB 661 TLLWKPLMKNDLSVQRYVINIHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI 720

QY 721 GASVANFNLTFSMPKSVKNTVQSLASVPLNSCVIVSWILSPDSYKLMYPIIEWKNLNED 780
DB 721 GASVANFNLTFSMPKSVKNTVQSLASVPLNSCVIVSWILSPDSYKLMYPIIEWKNLNED 780

QY 781 GEIKWLRISSSVKKYTHGKF 801
DB 781 GEIKWLRISSSVKKYTHGKF 801

QY 779 DGMKWLRISSSVKKYTHGKF 799
DB 779 DGMKWLRISSSVKKYTHGKF 799

RESULT 4

S68440
leptin receptor, splice form Ob-Rd - mouse
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 31-Dec-2000
C:Accession: S68440
R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; et al.
Nature 379, 632-635, 1996
A:Title: Abnormal splicing of the leptin receptor in diabetic mice.
A:Reference number: S68437; MUID:96231997
A:Accession: S68440

A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-900 <LEE>
A:Cross-references: EMBL:U49109; NID:g1195490; PIDN:AAC52423.1; PID:g1195491
A:Experimental source: tissue hypothalamus
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:
C:Genetics:
A:Gene: Ob-Rd
C:Keywords: alternative splicing; appetite; transmembrane protein
F:840-860/Domain: transmembrane #status predicted <TM>

Query Match 76.7%; Score 3345; DB 2; Length 900;
Best Local Similarity 76.0%; Pred. No. 3.le-226;
Matches 609; Conservative 73; Mismatches 117; Indels 2; Gaps 2;

QY 1 MICQFCVLLHWEFIYVITAFNLSYPTTPWRKFLSCMPNNTSYDYFLLPAGLSKNTSNS 60
DB 1 MMCQKFYVLLHWEFLYIAALNLAISPWKFLFCGPPNTDDSFSLPAGAPNNSAL 60

QY 61 NGHYETAPEKFNSSGTHFNLSKTFHCCFRSBDNRCSLCAONIEGKTFVTSVLSVF 120
DB 61 KGASEAIVEAKFNSSGIYVPELSKTFVHCCFNGQNGCSALTONTGKTLASVVKASVF 120

QY 121 QOIDANNIOCLKGLDKLFICYVESLFKNLFNRYNKKVHLLYVLPVLEDSPLVPKGS 180
DB 121 ROLGVNWDIECMKMGDLTLFICHMEPLKPNFKNYDSKVHLLYDLPVIDDSPLPLKDS 180

QY 181 FQVHCNSVHECCLECLVPVPTAKLNDTLMLCKLITSGVTFQSPMLSVQPINVKPDP 240
DB 181 FQVHCNSVHECCLECLVPVPTAKLNDTLMLCKLITSGVTFQSPMLSVQPINVKPDP 240

QY 241 LGLHMEITDDGNLKSWSPPPLVFPFLOQYQVYKYSNSTVIREADKIVSATSLLVDSILP 300
DB 241 LGLHMEITDDGNLKSWSPPPLVFPFLOQYQVYKYSNSTVIREADKIVSATSLLVDSILP 300

QY 301 GSSYEVOVRKRLDGLGYSVNSWSPATVYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
DB 301 GSSYEVOVRKRLDGLGYSVNSWSPATVYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660

QY 661 TLLWKPLMKNDLSVQRYVINIHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI 720
DB 661 TLLWKPLMKNDLSVQRYVINIHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI 720

QY 721 GASVANFNLTFSMPKSVKNTVQSLASVPLNSCVIVSWILSPDSYKLMYPIIEWKNLNED 780
DB 721 GASVANFNLTFSMPKSVKNTVQSLASVPLNSCVIVSWILSPDSYKLMYPIIEWKNLNED 780

QY 781 GEIKWLRISSSVKKYTHGKF 801
DB 781 GEIKWLRISSSVKKYTHGKF 801

QY 779 DGMKWLRISSSVKKYTHGKF 799
DB 779 DGMKWLRISSSVKKYTHGKF 799

RESULT 5
S68438
leptin receptor, splice form Ob-Rb - mouse
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1998 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000
C:Accession: S68438; S68441
R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; et al
Nature 379, 632-635, 1996
A:Title: Abnormal splicing of the leptin receptor in diabetic mice.
A:Reference number: S68437; MUID:96231937
A:Accession: S68438
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 664-1162 <LEE1>
A:Cross-references: EMBL:049107; NID:g1195486; PIDN:AAC52424.1; PID:g1195487
A:Experimental source: splice form Rb; tissue hypothalamus
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
A:Note: only a part of the translation is shown
A:Accession: S68441
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-796, GNCVLPMD' <LEE2>
A:Cross-references: EMBL:049110; NID:g1195492; PIDN:AAC52424.1; PID:g1195493
A:Experimental source: splice form Re; tissue hypothalamus
A:Note: this nucleotide sequence was submitted to the EMBL Data Library, February 1996
A:Note: the sequence from splice form Re is included to produce a complete sequence
C:Comment: for alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:S68440
C:Genetics:
A:Gene: Ob-Rb
C:Keywords: alternative splicing; appetite

Query Match 76.7%; Score 3345; DB 2; Length 1162;
Best Local Similarity 76.0%; Pred. No. 4.4e-226;
Matches 609; Conservative 73; Mismatches 117; Indels 2; Gaps 2;

QY 1 MICQKFCVLLHWEITVITAFNLSTYPTIPWFKLSCMPNSTYDYELLPAGLSKNTS 60
Db 1 MICQKFCVLLHWEITVITAFNLSTYPTIPWFKLSCMPNSTYDYELLPAGLSKNTS 60
QY 61 NGHYETAVEPKNSGTHFSNLSTKTHFCFSEQDRNCSLCAIDIEGKTFVSTVNSLVF 120
Db 61 KGASEAIVEAKFNSSGIYVPELSKTVFHCCEGQEQNSALTONTEGKTLASVVKASVF 120
QY 121 QOIDANNWIOCKLGLKLFICYVESLEKFNFRNYNKVHLLYVLPVLEDSPLVPQKGS 180
Db 121 ROLGVNWDIECMKGDGLTFICHMEPELPKPNPKYDYSKVHLLYDLPVLEDSPLVPQKGS 180
QY 181 FQVHCNCSVHECCBCLVPVPTAKLNDTLMLCKLITSGGVIFQSPFLMSVQPINVKPDPP 240
Db 181 FQVHCNCSVHECCBCLVPVPTAKLNDTLMLCKLITSGGVIFQSPFLMSVQPINVKPDPP 240
QY 241 LGLHMEITDDGNLKSWSPLPFPPLQYQVYKYSNSTTIVREADKIVSATSLLDVSLP 300
Db 241 LGLHMEITDDGNLKSWSPLPFPPLQYQVYKYSNSTTIVREADKIVSATSLLDVSLP 300
QY 301 GSSVEVQVRGRDLGPGTWSQSWSPRFTTQDYIFPPKILTSVGSNNVSHCIYKKNKI 360
Db 301 GSSVEVQVRGRDLGPGTWSQSWSPRFTTQDYIFPPKILTSVGSNNVSHCIYKKNKI 360
QY 361 VPSKEIVWMNLAKIPQSDVYVSDRVSKVTFEENLNKTPRGKFTYDVAVCCNEHCCH 420
Db 361 VPSKEIVWMNLAKIPQSDVYVSDRVSKVTFEENLNKTPRGKFTYDVAVCCNEHCCH 420
QY 421 RYAEYVIDVNIINISCTDGYLTWKTCTWSTSTIQSLAESTLQRYHRSLSYCDIPSII 480
Db 421 RYAEYVIDVNIINISCTDGYLTWKTCTWSTSTIQSLAESTLQRYHRSLSYCDIPSII 480
QY 481 PISPKDCYQSDGFCYICQIPILLSGYTWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
Db 481 PISPKDCYQSDGFCYICQIPILLSGYTWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
QY 540 PTSEPKNCVLQDGFYECVQPIFLLSGYTWIRINHSGLSDSPPTCVLPDSVVKPLPP 538
Db 540 PTSEPKNCVLQDGFYECVQPIFLLSGYTWIRINHSGLSDSPPTCVLPDSVVKPLPP 538

QY 541 SSVKAETITNIGLLKISWEKPPENNLOFOIRYGLSGKEVQWKMVEYVDKSKSVLPV 600
Db 539 SSVKAETITNIGLLKISWEKPPENNLOFOIRYGLSGKEVQWKMVEYVDKSKSVLPV 598
QY 601 PDICAVAVOVRCKRDLGLGYGWSNPNPAYTVVYMDIKVPMRGPEFWRIINGDPMKKEKNV 660
Db 599 SDICAVAVOVRCKRDLGLGYGWSNPNPAYTVVYMDIKVPMRGPEFWRIINGDPMKKEKNV 658
QY 661 TLWKKPLMKNDSCSVORVYVNIHHTSCNGTWSDEDVGNHKTFTFLWTEQAHVTVLAINSI 720
Db 659 TLWKKPLMKNDSCSVORVYVNIHHTSCNGTWSDEDVGNHKTFTFLWTEQAHVTVLAINSI 718
QY 721 GASVANFNLTFSWPMKSVNIQSLAYSAYPLNSCVIVSWILSPSDYKLMYFIETWKNLNEED 780
Db 719 GASVANFNLTFSWPMKSVNIQSLAYSAYPLNSCVIVSWILSPSDYKLMYFIETWKNLNEED 778
QY 781 GEIKWLRISSVKKYIHKGF 801
Db 779 DGMKKWLRIPSNNYKFIHDF 799
RESULT 6
PC4184
leptin receptor, Ob-Rb - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 01-Dec-2000
C:Accession: JC4895; JC4896; JC4897; PC4184; JC4797
R:Takaya, K.; Ogawa, Y.; Isse, N.; Okazaki, T.; Satoh, N.; Masuzaki, H.; Mori, K.; et al
Biochem. Biophys. Res. Commun. 225, 75-83, 1996
A:Title: Molecular cloning of rat leptin receptor isoform complementary DNAs-identifi
A:Reference number: JC4895; MUID:96332408
A:Accession: JC4895
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1162 <TA3>
A:Cross-references: DDBJ:D85558; NID:g1526441; PIDN:BAAL2831.1; PID:d1013515; PID:g15
A:Accession: JC4896
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-889, 'RADTL' <TA2>
A:Cross-references: DDBJ:D85557
A:Accession: JC4897
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-796, 'G', 1157-1158, 'TVLLN' <TA3>
A:Cross-references: DDBJ:D85559
R:Iida, M.; Murakami, T.; Ishida, K.; Mizuno, A.; Kuwajima, M.; Shima, K.
Biochem. Biophys. Res. Commun. 224, 597-604, 1996
A:Title: Substitution at codon 269 (glutamine-proline) of the leptin receptor (OB-R)
A:Reference number: PC4184; MUID:96295531
A:Accession: PC4184
A:Molecule type: mRNA
A:Residues: 840-1162 <IID>
A:Cross-references: DDBJ:D84550
R:Iida, M.; Murakami, T.; Ishida, K.; Mizuno, A.; Kuwajima, M.; Shima, K.
Biochem. Biophys. Res. Commun. 222, 19-26, 1996
A:Title: Phenotype-linked amino acid alteration in leptin receptor cDNA from Zucker f
A:Reference number: JC4797; MUID:96212906
A:Accession: JC4797
A:Molecule type: mRNA
A:Residues: 1-889, 'RADTL' <IID>
A:Cross-references: DDBJ:D84125; NID:g1374707; PIDN:BAAL2230.1; PID:g1374708
A:Experimental source: adipose cell
C:Comment: This receptor is obese-phenotype-linked mutant, found in the Zucker (fa/fa
C:Genetics:
A:Gene: fa
C:Keywords: appetite; transmembrane protein
F:840-860/Domain: transmembrane #status predicted <TM>
F:861-1162/Domain: intracellular #status predicted <INT>

Query Match 76.6%; Score 3342; DB 2; Length 1162;
Best Local Similarity 76.0%; Pred. No. 7.1e-226;

Matches 609; Conservative 74; Mismatches 116; Indels 2; Gaps 2;

QY 1 MTCQKFCVLLHWEFYVITAFNLSPYTPWRFKLSMPPNSTYDFLLPAGLSKNTS 60
 Db 1 MTCQKFCVLLHWEFYVITAFNLSPYTPWRFKLSMPPNSTYDFLLPAGLSKNTS 60
 QY 61 NGHETAVPEKNSGTHFNSLTKTFHCCFSEQRNCSLACADNIEGKTFVSTVNSL 120
 Db 61 KGASEALVEAKFNSTGIYVSELSKTFHCCFSEQRNCSLACADNIEGKTFVSTVNSL 120
 QY 121 QOITANWNIQCKLGLKLFICYVESLFKNFRNRYNKHVLLYVLEVDSPVPKGS 180
 Db 121 ROLGVNWDIECKMKGDLTFLFICHMEPLLNPKYDKSVHLLYDLPEVDDLPPLKDS 180
 QY 181 FQVHCNCSVECECCCLVPVPTAKLNDTLLMCLKITSGVIFQSPMSVQPINMYKPP 240
 Db 181 FQVHCNCSVECECCCLVPVPTAKLNDTLLMCLKITSGVIFQSPMSVQPINMYKPP 240
 QY 181 FQVHCNCSVECECCCLVPVPTAKLNDTLLMCLKITSGVIFQSPMSVQPINMYKPP 240
 Db 181 FQVHCNCSVECECCCLVPVPTAKLNDTLLMCLKITSGVIFQSPMSVQPINMYKPP 240
 QY 241 LGLHMEITDDGNLKSWSQTPKAPPLQVQVYKYSNSTVIREADKIYSATSLVDSILP 300
 Db 241 LGLHMEITDDGNLKSWSQTPKAPPLQVQVYKYSNSTVIREADKIYSATSLVDSILP 300
 QY 241 LGLHMEITDDGNLKSWSQTPKAPPLQVQVYKYSNSTVIREADKIYSATSLVDSILP 300
 Db 241 LGLHMEITDDGNLKSWSQTPKAPPLQVQVYKYSNSTVIREADKIYSATSLVDSILP 300
 QY 301 GSSYEVQVGRKLDGPGIWSDMSTPRVFTTQDVYFPFKILTSGVSNVSHFCHYKKNKI 360
 Db 301 GSSYEVQVGRKLDGPGIWSDMSTPRVFTTQDVYFPFKILTSGVSNVSHFCHYKKNKI 360
 QY 301 GSSYEVQVGRKLDGPGIWSDMSTPRVFTTQDVYFPFKILTSGVSNVSHFCHYKKNKI 360
 Db 301 GSSYEVQVGRKLDGPGIWSDMSTPRVFTTQDVYFPFKILTSGVSNVSHFCHYKKNKI 360
 QY 361 VPSKEIIVMMNLAEKIPQSDVSDHVSQVTKFFNLNETKPRGKFTYDAVYCCNECHH 420
 Db 361 VPSKEIIVMMNLAEKIPQSDVSDHVSQVTKFFNLNETKPRGKFTYDAVYCCNECHH 420
 QY 361 VPSKEIIVMMNLAEKIPQSDVSDHVSQVTKFFNLNETKPRGKFTYDAVYCCNECHH 420
 Db 361 VPSKEIIVMMNLAEKIPQSDVSDHVSQVTKFFNLNETKPRGKFTYDAVYCCNECHH 420
 QY 421 RYAEIYVDVNIINISCTDGYLTMTKCRWSTIQLAESTLQRLYHRSLSYCDIPSIH 480
 Db 421 RYAEIYVDVNIINISCTDGYLTMTKCRWSTIQLAESTLQRLYHRSLSYCDIPSIH 480
 QY 421 RYAEIYVDVNIINISCTDGYLTMTKCRWSTIQLAESTLQRLYHRSLSYCDIPSIH 480
 Db 421 RYAEIYVDVNIINISCTDGYLTMTKCRWSTIQLAESTLQRLYHRSLSYCDIPSIH 480
 QY 481 PISEPKCYLQSDGFEYECIFQIFLLSGYTMIRINHSLSGSDSPCTCLPDSVVKPLPP 540
 Db 481 PISEPKCYLQSDGFEYECIFQIFLLSGYTMIRINHSLSGSDSPCTCLPDSVVKPLPP 540
 QY 481 PISEPKCYLQSDGFEYECIFQIFLLSGYTMIRINHSLSGSDSPCTCLPDSVVKPLPP 540
 Db 481 PISEPKCYLQSDGFEYECIFQIFLLSGYTMIRINHSLSGSDSPCTCLPDSVVKPLPP 540
 QY 479 PISEPKCYLQSDGFEYECIFQIFLLSGYTMIRINHSLSGSDSPCTCLPDSVVKPLPP 538
 Db 479 PISEPKCYLQSDGFEYECIFQIFLLSGYTMIRINHSLSGSDSPCTCLPDSVVKPLPP 538
 QY 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSKEVQWKMVEYDAKSKSVSLPV 600
 Db 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSKEVQWKMVEYDAKSKSVSLPV 600
 QY 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSKEVQWKMVEYDAKSKSVSLPV 600
 Db 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSKEVQWKMVEYDAKSKSVSLPV 600
 QY 539 SNVKAETINTGLKLVSWKVPFPENNLOFQIRYGLSKEVQWKMVEYDAKSKSVSLPV 598
 Db 539 SNVKAETINTGLKLVSWKVPFPENNLOFQIRYGLSKEVQWKMVEYDAKSKSVSLPV 598
 QY 601 PDLCAVAVQVRCRDLGLGYWNSNPAYTVMDIKVPMRGPEFWRINGDTHKKEKNV 660
 Db 601 PDLCAVAVQVRCRDLGLGYWNSNPAYTVMDIKVPMRGPEFWRINGDTHKKEKNV 660
 QY 601 PDLCAVAVQVRCRDLGLGYWNSNPAYTVMDIKVPMRGPEFWRINGDTHKKEKNV 660
 Db 601 PDLCAVAVQVRCRDLGLGYWNSNPAYTVMDIKVPMRGPEFWRINGDTHKKEKNV 660
 QY 599 SDCAVYVQVRCRDLGLGYWNSNPAYTVMDIKVPMRGPEFWRINGDTHKKEKNV 658
 Db 599 SDCAVYVQVRCRDLGLGYWNSNPAYTVMDIKVPMRGPEFWRINGDTHKKEKNV 658
 QY 661 TLLMKPLMKNDLSLCSVQRYVINHHSTSCNGTWSDEYGNHKTFTFLWTEQAHVTVLAINSI 720
 Db 661 TLLMKPLMKNDLSLCSVQRYVINHHSTSCNGTWSDEYGNHKTFTFLWTEQAHVTVLAINSI 720
 QY 661 TLLMKPLMKNDLSLCSVQRYVINHHSTSCNGTWSDEYGNHKTFTFLWTEQAHVTVLAINSI 720
 Db 661 TLLMKPLMKNDLSLCSVQRYVINHHSTSCNGTWSDEYGNHKTFTFLWTEQAHVTVLAINSI 720
 QY 659 TLLMKPLMKNDLSLCSVQRYVINHHSTSCNGTWSDEYGNHKTFTFLWTEQAHVTVLAINSI 718
 Db 659 TLLMKPLMKNDLSLCSVQRYVINHHSTSCNGTWSDEYGNHKTFTFLWTEQAHVTVLAINSI 718
 QY 721 GASVANFNLTSPWPMKYNVQSLGAYPLNSSCVIVSWILSPSDYKLMFYIEKNLND 780
 Db 721 GASVANFNLTSPWPMKYNVQSLGAYPLNSSCVIVSWILSPSDYKLMFYIEKNLND 780
 QY 719 GASLVNFNLTSPWPMKYNVQSLGAYPLNSSCVIVSWILSPSDYKLMFYIEKNLND 778
 Db 719 GASLVNFNLTSPWPMKYNVQSLGAYPLNSSCVIVSWILSPSDYKLMFYIEKNLND 778
 QY 781 GEIKWLRTSSSVKYYIHGKF 801
 Db 781 GEIKWLRTSSSVKYYIHGKF 801
 QY 779 DGMKWLRIPSNVNYYIHDF 799
 Db 779 DGMKWLRIPSNVNYYIHDF 799

RESULT 7

S74225

leptin receptor, isoform Ob-Rf - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 05-Nov-1999

C:Accession: S74225

R:Wang, M.Y.; Zhou, Y.T.; Newgard, C.B.; Unger, R.H.

FEBS Lett. 392, 87-90, 1996

A:Title: A novel leptin receptor isoform in rat.

A:Reference number: S74225; MUID:96368027

A:Accession: S74225

A:Molecule type: mRNA

A:Residues: 1-895 <WAN>

A:Cross-references: EMBL:U53144; NID:g1395212; PIDN:AAB03088.1; PID:g1395213

A:Experimental source: strain Sprague-Dawley; tissue type brain
 C:Genetics:
 A:Gene: rob-R
 C:Keywords: appetite; transmembrane protein
 F:840-860/Domain: transmembrane #status predicted <TM>

Query Match 75.3%; Score 3284; DB 2; Length 895;
 Best Local Similarity 75.0%; Pred. No. 5.7e-222;
 Matches 601; Conservative 77; Mismatches 121; Indels 2; Gaps 2;

QY 1 MTCQKFCVLLHWEFYVITAFNLSPYTPWRFKLSMPPNSTYDFLLPAGLSKNTS 60
 Db 1 MTCQKFCVLLHWEFYVITAFNLSPYTPWRFKLSMPPNSTYDFLLPAGLSKNTS 60
 QY 61 NGHETAVPEKNSGTHFNSLTKTFHCCFSEQRNCSLACADNIEGKTFVSTVNSL 120
 Db 61 KGASEALVEAKFNSTGIYVSELSKTFHCCFSEQRNCSLACADNIEGKTFVSTVNSL 120
 QY 121 QOITANWNIQCKLGLKLFICYVESLFKNFRNRYNKHVLLYVLEVDSPVPKGS 180
 Db 121 ROLGVNWDIECKMKGDLTFLFICHMEPLLNPKYDKSVHLLYDLPEVDDLPPLKDS 180
 QY 181 FQVHCNCSVECECCCLVPVPTAKLNDTLLMCLKITSGVIFQSPMSVQPINMYKPP 240
 Db 181 FQVHCNCSVECECCCLVPVPTAKLNDTLLMCLKITSGVIFQSPMSVQPINMYKPP 240
 QY 181 FQVHCNCSVECECCCLVPVPTAKLNDTLLMCLKITSGVIFQSPMSVQPINMYKPP 240
 Db 181 FQVHCNCSVECECCCLVPVPTAKLNDTLLMCLKITSGVIFQSPMSVQPINMYKPP 240
 QY 241 LGLHMEITDDGNLKSWSQTPKAPPLQVQVYKYSNSTVIREADKIYSATSLVDSILP 300
 Db 241 LGLHMEITDDGNLKSWSQTPKAPPLQVQVYKYSNSTVIREADKIYSATSLVDSILP 300
 QY 241 LGLHMEITDDGNLKSWSQTPKAPPLQVQVYKYSNSTVIREADKIYSATSLVDSILP 300
 Db 241 LGLHMEITDDGNLKSWSQTPKAPPLQVQVYKYSNSTVIREADKIYSATSLVDSILP 300
 QY 301 GSSYEVQVGRKLDGPGIWSDMSTPRVFTTQDVYFPFKILTSGVSNVSHFCHYKKNKI 360
 Db 301 GSSYEVQVGRKLDGPGIWSDMSTPRVFTTQDVYFPFKILTSGVSNVSHFCHYKKNKI 360
 QY 301 GSSYEVQVGRKLDGPGIWSDMSTPRVFTTQDVYFPFKILTSGVSNVSHFCHYKKNKI 360
 Db 301 GSSYEVQVGRKLDGPGIWSDMSTPRVFTTQDVYFPFKILTSGVSNVSHFCHYKKNKI 360
 QY 361 VPSKEIIVMMNLAEKIPQSDVSDHVSQVTKFFNLNETKPRGKFTYDAVYCCNECHH 420
 Db 361 VPSKEIIVMMNLAEKIPQSDVSDHVSQVTKFFNLNETKPRGKFTYDAVYCCNECHH 420
 QY 361 VPSKEIIVMMNLAEKIPQSDVSDHVSQVTKFFNLNETKPRGKFTYDAVYCCNECHH 420
 Db 361 VPSKEIIVMMNLAEKIPQSDVSDHVSQVTKFFNLNETKPRGKFTYDAVYCCNECHH 420
 QY 421 RYAEIYVDVNIINISCTDGYLTMTKCRWSTIQLAESTLQRLYHRSLSYCDIPSIH 480
 Db 421 RYAEIYVDVNIINISCTDGYLTMTKCRWSTIQLAESTLQRLYHRSLSYCDIPSIH 480
 QY 421 RYAEIYVDVNIINISCTDGYLTMTKCRWSTIQLAESTLQRLYHRSLSYCDIPSIH 480
 Db 421 RYAEIYVDVNIINISCTDGYLTMTKCRWSTIQLAESTLQRLYHRSLSYCDIPSIH 480
 QY 481 PISEPKCYLQSDGFEYECIFQIFLLSGYTMIRINHSLSGSDSPCTCLPDSVVKPLPP 540
 Db 481 PISEPKCYLQSDGFEYECIFQIFLLSGYTMIRINHSLSGSDSPCTCLPDSVVKPLPP 540
 QY 481 PISEPKCYLQSDGFEYECIFQIFLLSGYTMIRINHSLSGSDSPCTCLPDSVVKPLPP 540
 Db 481 PISEPKCYLQSDGFEYECIFQIFLLSGYTMIRINHSLSGSDSPCTCLPDSVVKPLPP 540
 QY 479 PISEPKCYLQSDGFEYECIFQIFLLSGYTMIRINHSLSGSDSPCTCLPDSVVKPLPP 538
 Db 479 PISEPKCYLQSDGFEYECIFQIFLLSGYTMIRINHSLSGSDSPCTCLPDSVVKPLPP 538
 QY 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSKEVQWKMVEYDAKSKSVSLPV 600
 Db 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSKEVQWKMVEYDAKSKSVSLPV 600
 QY 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSKEVQWKMVEYDAKSKSVSLPV 600
 Db 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSKEVQWKMVEYDAKSKSVSLPV 600
 QY 539 SNVKAETINTGLKLVSWKVPFPENNLOFQIRYGLSKEVQWKMVEYDAKSKSVSLPV 598
 Db 539 SNVKAETINTGLKLVSWKVPFPENNLOFQIRYGLSKEVQWKMVEYDAKSKSVSLPV 598
 QY 601 PDLCAVAVQVRCRDLGLGYWNSNPAYTVMDIKVPMRGPEFWRINGDTHKKEKNV 660
 Db 601 PDLCAVAVQVRCRDLGLGYWNSNPAYTVMDIKVPMRGPEFWRINGDTHKKEKNV 660
 QY 601 PDLCAVAVQVRCRDLGLGYWNSNPAYTVMDIKVPMRGPEFWRINGDTHKKEKNV 660
 Db 601 PDLCAVAVQVRCRDLGLGYWNSNPAYTVMDIKVPMRGPEFWRINGDTHKKEKNV 660
 QY 599 SDCAVYVQVRCRDLGLGYWNSNPAYTVMDIKVPMRGPEFWRINGDTHKKEKNV 658
 Db 599 SDCAVYVQVRCRDLGLGYWNSNPAYTVMDIKVPMRGPEFWRINGDTHKKEKNV 658
 QY 661 TLLMKPLMKNDLSLCSVQRYVINHHSTSCNGTWSDEYGNHKTFTFLWTEQAHVTVLAINSI 720
 Db 661 TLLMKPLMKNDLSLCSVQRYVINHHSTSCNGTWSDEYGNHKTFTFLWTEQAHVTVLAINSI 720
 QY 661 TLLMKPLMKNDLSLCSVQRYVINHHSTSCNGTWSDEYGNHKTFTFLWTEQAHVTVLAINSI 720
 Db 661 TLLMKPLMKNDLSLCSVQRYVINHHSTSCNGTWSDEYGNHKTFTFLWTEQAHVTVLAINSI 720
 QY 659 TLLMKPLMKNDLSLCSVQRYVINHHSTSCNGTWSDEYGNHKTFTFLWTEQAHVTVLAINSI 718
 Db 659 TLLMKPLMKNDLSLCSVQRYVINHHSTSCNGTWSDEYGNHKTFTFLWTEQAHVTVLAINSI 718
 QY 721 GASVANFNLTSPWPMKYNVQSLGAYPLNSSCVIVSWILSPSDYKLMFYIEKNLND 780
 Db 721 GASVANFNLTSPWPMKYNVQSLGAYPLNSSCVIVSWILSPSDYKLMFYIEKNLND 780
 QY 719 GASLVNFNLTSPWPMKYNVQSLGAYPLNSSCVIVSWILSPSDYKLMFYIEKNLND 778
 Db 719 GASLVNFNLTSPWPMKYNVQSLGAYPLNSSCVIVSWILSPSDYKLMFYIEKNLND 778
 QY 781 GEIKWLRTSSSVKYYIHGKF 801
 Db 781 GEIKWLRTSSSVKYYIHGKF 801
 QY 779 DGMKWLRIPSNVNYYIHDF 799
 Db 779 DGMKWLRIPSNVNYYIHDF 799

RESULT 8

I49699

glycoprotein 130 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Jul-2000

C:Accession: I49699; I48370
R:Saito, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.
J. Immunol. 148, 4066-4071, 1992
A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp130
A:Reference number: I48370; MUID:92291532
A:Accession: I49699
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <RES>
A:Cross-references: GB:M83336; NID:g193591; PIDN:AAA37723.1; PID:g193592
A:Map position: 5q11-5q11
A:Superfamily: cytokine receptor homology
A:Keywords: glycoprotein
F:134-314/Domain: cytokine receptor homology <CRS>
Query Match 6.8%; Score 296; DB 2; Length 917;
Best Local Similarity 22.8%; Pred. No. 9.5e-13;
Matches 121; Conservative 95; Mismatches 214; Indels 100; Gaps 26;
QY 323 STPRVFTTQDIYE-----PPKILTSVGSNVSFHCYKK---ENKIVP 362
DB 2 SAPRIWLAQLFFUTTESIGOLLEPCGYIPEFVQVQSGNFTALCVLKEACLAQHYYN 61
QY 363 SKEIYWMNLAEPQSQVDVSDHVKVTFNENLTPRGKFTYDAVYCCNEHECHRY 422
DB 62 ASYIVKTNHA-AVPREQVTINRTTSSVTFDVA-VLPVOLT-----CNILSFGQIE 112
QY 423 AELVYI-----DVNINISC-ETDGYLTMTKRWSTSTIOSLAESTIQLRYHRSLLYC 473
DB 113 QNVYGVTMLSGPPDPKPTNLTCIVNEG--KNMLCQWDPG-----RETLETNYTLKSEWA 165
QY 474 SDIPSIIPISEPKCYLQSDGFYECI--FQPIFLSGYTMIRINHSGLSDSPPTCVLP 531
DB 166 TE-----FPDCC--QSKHGTSVMVSYTYVYN-IEVWVEAENALGKVSSEINFD 214
QY 532 DSVVKPLPSSVKAETITNI-GLLIIISKEKVPENNLFQFIRYGLSG-----KVQV--- 582
DB 215 VDKVKPTPYNLSTVNSLSILKLSW-----VSSGIGLLDLKSDIYRT 261
QY 583 -----WKMEYVDKAKSVSLPVPDL--CAVYAVQVRCRLDGLGYSNWSNPAYTVMD 635
DB 262 KDASTWIOVPLEDTMSRPTSTFVQDLKPTFTEYVFRIRSIKDGKGYSDWSEASGTYE 321
QY 636 IKVPMRGPFWRIINGDTMKKEKNVTLWPKMNDLSQVQRY--VINHHTSCNGTWSE 693
DB 322 DR-PSRPPSFYKTNPSHGQYRSVRLIWKALPLSEANGKILDYEIVLTQSKVSQTYTV 380
QY 694 DVGHTKFTFLWTEQAHVTIVLAINSIGAVANENLFSWP-MSKVNIVQSLAYPLNS 752
DB 381 ---TGELTVNLNDRYVAVSLAARKVKGSAAV-LTIPSPHTVAAYSVNWKAPP-KDN 435
QY 753 CVIVSWILSPSDYKLMYFIIEKWNLEDGEI--KWLRISSSVKYYIHGK 800
DB 436 LLWVEW--TPPKPKVYILEWCVLSENAPCVEDWQEDATVNTHLRGR 483
RESULT 9
membrane glycoprotein gp130 precursor - human
C:Species: Homo sapiens (man)
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 28-Jul-2000
C:Accession: A36337
R:Hibi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.
Cell 63, 1149-1157, 1990
A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A:Reference number: A36337; MUID:91084844

A:Accession: A36337
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-918 <HIB>
A:Cross-references: GB:M57230; NID:g186353; PIDN:AAA59155.1; PID:g186354
C:Genetics: GDB:IL6ST; GPI30
A:Gene: GDB:IL6ST; GPI30
A:Cross-references: GDB:126725; OMIM:600694
A:Map position: 5q11-5q11
A:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; membrane protein
F:134-316/Domain: cytokine receptor homology <CRS>

Query Match 6.4%; Score 271.5; DB 2; Length 918;
Best Local Similarity 22.7%; Pred. No. 1.9e-11;
Matches 112; Conservative 82; Mismatches 227; Indels 73; Gaps 22;
QY 337 PPKILTSVGSNVSFHCYKK---ENKIVPSKEIVWMNLAEPQSQVDVSDHVKVTF 393
DB 33 PESPVQLHSNFTAVCVLKEKCMDFHVNANYVKTN-HFTIPKEQVTIINRTASSVTF 91
QY 394 ENLNETKPRGFTYDAVYCCNEHECHRYAELVYIDV-----NINISC-ETDGYLT 444
DB 92 TDI-----ASLNIQTICNLITFGQLEQNVYITIIISGLPPEKPKNLSCIVNEG--KK 141
QY 445 MTCRWSTSTIOSLAESTIQLRYHRSLLYCSIDIPSIHPISPEKDCYLOSDGFYECI--FOP 502
DB 142 MRCWDGG-----RETHLETNFTLSEWAT-----HKFA---DCKAKRDTPTSCVTDYST 188
QY 503 IFLSGYTMIRINHSGLSDSPPTCVLPDSVVKPLPSSVKAETITN-----IGLLKISW 558
DB 189 VYFVN-IEVWVEAENALGKVTSDHINFDPVYKVPNPPHLS---VINSEELSLTLKLTW 244
QY 559 EKP-----VPENNLFQFIRYGLSKKEVQWMEYVDYDAKSVSLPVPDL--CAVYAVQV 611
DB 245 TNPISKSVIILKYNIOYRTKDAST-----WSQIPEDPASTRSSFTVQDLKPFTEYVERI 299
QY 612 RCKRLDGLGYSNWSNPAYTVVMDIKVPMRGPFWRIINGDTMKKEKNVTLWPKLMD 671
DB 300 RCMKEDCKGYSDWSEASGITYEDR-PSKAPSFYKIDPSTHOGYRTVQLVWKTLPPFE 358
QY 672 SLCSVQRYVINHHTSCNGTWSVDGNH---TKFTLWTEQAHVTIVLAINSIGAVANF 727
DB 359 ANGKILDYEV-----LTRWKSHLQNTVNTATKLTNLTNDRYLATLTVRNLVSKDAV 413
QY 728 NLTFSPWPKSVNIQSLAYSAYPLNSCVISVLSILSPSDYKLMYFIIEKWNLEDGE--IKW 785
DB 414 LTIPACDFQATHPYMDLKAFP-KDNMLMVEWTTTPRESVK--KYILEWCVLSDKAPCIITDW 470
QY 786 LRISSSVKYYIHG 799
DB 471 QOEDGTVHRTYLRG 484

RESULT 10
A44257
interleukin-6 signal transducing molecule gp130 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 28-Jul-2000
C:Accession: A44257
R:Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.
Genomics 14, 666-672, 1992
A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transducer
A:Reference number: A44257; MUID:93052397
A:Accession: A44257
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-918 <WAN>
A:Experimental source: liver
A:Note: sequence extracted from NCBI backbone (NCBI:118488)
C:Superfamily: cytokine receptor homology
C:Keywords: transmembrane protein

db 91 PHLNVTQ---AFLFCLVPWEDSVQLLDQAEHLHAGYPPA---SPENLSCLMLHLTTNSLVC 143

Qy 602 -DLCAV-----YAVQVRCRRKLDGLGWSNWSNPAYTVVWMDIKVPMRGP-----EFWRRIIN 650
:||: | :||| | :||| | : :|| | :||
244 YASCLQDQWE FWFQGHJHAWCEBUNIRFQNGRSMADVO -PUEERLQ 250

Db 292 YELGGLPATATYTLQIRCMPLPGHSDWS-PS-----LELRTTERTAPTVRDLTWRR--- 343
QY 651 GDTMKKEKNVTLLMKPLKNDLSQVQRYVNLHRTS-----CNGTWSDEVGNHTKF 701
Db 344 -OROLDPRTVLFKPKVPLEDSGRIOGYVSWRPQAGAILPLCNTT-----ELSC 395
QY 702 TFLWTEQATVTVLAINSIGASVANFNLTFSWPKSKYNIVQSLSAYPLNNSCVIVSWILS 761
Db 396 TFHLPSEAQVALVAYNSAGTSRPT-PVVFES--ESRGPALTRLHAMARDPHSLMWGM--E 450
QY 762 PSDYKLMVFIIEW 774
Db 451 PPNWPQGYVIEW 463

RESULT 13
JH0329
granulocyte colony-stimulating factor receptor D7 precursor - human
C:Species: Homo sapiens (man)
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-Nov-1999
R:Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.; Son
J. Exp. Med. 172, 1559-1570, 1990
A:Title: Expression cloning of a human granulocyte colony-stimulating factor receptor: a
A:Reference number: JH0329; MUID:91079757
A:Accession: JH0329
A:Molecule type: mRNA
A:Residues: 1-783 <LAR>
A:Cross-references: GB:M55720; NID:g31698; PIDN:CAA39252.1; PID:g31699
A:Experimental source: placenta
C:Keywords: glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-783/Product: granulocyte colony-stimulating factor receptor D7 #status predicted <F>
F:25-627/Domain: extracellular #status predicted <EXT>
F:628-653/Domain: transmembrane #status predicted <TRA>
F:654-783/Domain: intracellular #status predicted <INT>
F:93,128,134,389,474,579,610/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.6%; Score 242.5; DB 2; Length 783;
Best Local Similarity 22.7%; Pred. No. 4.3e-09;
Matches 112; Conservative 75; Mismatches 183; Indels 123; Gaps 25;

QY 341 LTSVGSNSVFCIYKKE-NKIVPSKEIYVMNLAEPKIQSQYDVVSD--HVSQVTFEFLN 397
Db 35 IVHLGDPITASCIKQNGSHLDPEQILRLG-AELQPGGRQRLSDGTQESITPLRLN 93
QY 398 ETKPRGKFTYDAVYCCNEHCHRYAEIYVID-----VNINISCTDGYLTGMT 446
Db 94 HTQ-----AFLSG-----CLNMGNSLIQILDQVELRAGYPPAIPHNLSCLMNLTTSLI 141
QY 447 CRWSTSTIQSLAES-TLQRYHRSLSYCDIPSHTPISEPKDCYLOSDGFVECI----- 499
Db 142 QWEPGPGPETHLPTSTLKSFRSG-----NCTQGDSDILDCVPKDGQS 184
QY 500 -----FQPIFLSSGYTWIRNHSLGSDSPPTCVLPDVSVKPLPP-----SSVRAEIT 548
Db 185 HCCIPRKHLLLYQNGIWIQVQAEALGTSMPQLCLDPMVVKLEPPMLRMTDPSPEA-AP 243
QY 549 INIGLLKISWEKVPFP-ENNLQFQIRYGLSGREVQVQKMYEVDAKSKSVSLPVP----- 601
Db 244 PQAGCLQLCHE-PWQGLGHNQKELRHKFPQGEASWALVG-----PLPLEALQ 291
QY 602 -DLCAV-----YAVQVCKRLDGLGYSWNSNPAYTVVMDIKVPMRCP-----EFWRILN 650
Db 292 YELGGLPATATYTLQIRCMPLPGHSDWS-PS-----LELRTTERTAPTVRDLTWRR--- 343
QY 651 GDTMKKEKNVTLLMKPLKNDLSQVQRYVNLHRTS-----CNGTWSDEVGNHTKF 701
Db 344 -OROLDPRTVLFKPKVPLEDSGRIOGYVSWRPQAGAILPLCNTT-----ELSC 395
QY 702 TFLWTEQATVTVLAINSIGASVANFNLTFSWPKSKYNIVQSLSAYPLNNSCVIVSWILS 761

Db 396 TFHLPSEAQVALVAYNSAGTSRPT-PVVFES--ESRGPALTRLHAMARDPHSLMWGM--E 450
QY 762 PSDYKLMVFIIEW 774
Db 451 PPNWPQGYVIEW 463

RESULT 14
C38252
granulocyte colony-stimulating factor receptor precursor, long form - human
N:Contains: granulocyte colony-stimulating factor, long form; granulocyte colony-stim
C:Species: Homo sapiens (man)
C>Date: 14-Jun-1991 #sequence_revision 30-Jan-1993 #text_change 05-Nov-1999
C:Accession: C38252; JH0330; A46486; S68332; S21607
R:Fukunaga, R.; Seto, Y.; Mizushima, S.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 8702-8706, 1990
A:Title: Three different mRNAs encoding human granulocyte colony-stimulating factor r
A:Reference number: A38252; MUID:91062348
A:Accession: C38252
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-863 <FUK>
A:Cross-references: GB:M59820; GB:M38027; NID:g183048; PIDN:AAA63178.1; PID:g183049
A>Note: Clones pHG11 and pHG5
A:Accession: A38252
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-680,708-863 <FU2>
A:Cross-references: GB:M59818; GB:M38025; NID:g183046; PIDN:AAA63176.1; PID:g183047
A>Note: clone pHQ3
R:Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.;
J. Exp. Med. 172, 1559-1570, 1990
A:Title: Expression cloning of a human granulocyte colony-stimulating factor receptor
A:Reference number: JH0329; MUID:91079757
A:Accession: JH0330
A:Molecule type: mRNA
A:Residues: 1-680,708-863 <LAR>
A:Cross-references: GB:X5721; NID:g31696; PIDN:CAA39253.1; PID:g31697
A>Note: clone 25-1; placenta
R:Seto, Y.; Fukunaga, R.; Nagata, S.
J. Immunol. 148, 259-266, 1992
A:Title: Chromosomal gene organization of the human granulocyte colony-stimulating fa
A:Reference number: A46486; MUID:92091782
A:Accession: A46486
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 855-863 <SET>
A:Cross-references: GB:S71484; NID:g240883; PIDN:AAB20660.1; PID:g240884
A:Experimental source: granulocyte
A>Note: sequence extracted from NCBI backbone (NCBIN:71484, NCBI:P:71485)
R:Haniu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F.
Arch. Biochem. Biophys. 324, 344-356, 1995
A:Title: Extracellular domain of granulocyte-colony stimulating factor receptor.
A:Reference number: S68331; MUID:96132662
A:Accession: S68332
A:Molecule type: protein
A:Residues: 234-269 <HAN>
C:Genetics:
A:Gene: GDB:CSF3R
A:Cross-references: GDB:126430; OMIM:138971
A:Map position: lp35-lp34.3
C:Keywords: alternative splicing; glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-863/Product: granulocyte colony-stimulating factor receptor, long form #status p
F:25-680,708-863/Product: granulocyte colony-stimulating factor receptor, short form
F:25-627/Domain: extracellular #status predicted <EXT>
F:628-653/Domain: transmembrane #status predicted <TRA>
F:654-863/Domain: intracellular #status predicted <INT>
F:93,128,134,389,474,579,610/Binding site: carbohydrate (Asn) (covalent) #status pred

Query Match 5.6%; Score 242.5; DB 2; Length 863;
Best Local Similarity 22.7%; Pred. No. 4.9e-09;

Matches 112; **Conservative** 75; **Mismatches** 183; **Indels** 123; **Gaps** 25;

QY	341	LTSGVSNVSHCYKKE-NKIVPSKEIIVWMNLAEKIPQSQDYDVSD--HVSQVTFNPLN	397
Db	35	IVHLGDPITACIKQNCSHLDPEQLWRLG-AELQGGQRQLSDCTQESIIITPLHN	93
QY	398	ETKPRGKFTYDAVCCNEHECHRYAELYVD-----VNINISCTDGYLFKMT	446
Db	94	HTQ-----AFLSC-----CLWNGNSLQILDQVELRAGYPPAIPHLNSCLMNIITSSLI	141
QY	447	CRMSTSTIQSLAES-TLQLRYHRSSLYCSDIPSHPISEPKDCYLQSDGFVECI-----	499
Db	142	CQWEPGPETHLPSTFLKSKSRG-----NCOTQGDSILDCVPKDGQS	184
QY	500	-----FQPIELSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP-----SSVKAET	548
Db	185	HCCIPRKHLLYQNGGIWQAENALGTSMSPOLCLDPMDVVKLEPPMLRTMDPSPEA-AP	243
QY	549	INTGLLKISKEKVPF--ENNLFQIRYGLSGREVQHKMYEYDAKSKSVSLVP-----	601
Db	244	PQAGCQLQWE-PWQPLGHHTNQCELRHKRQGEASWALVG-----PLPLEALQ	291
QY	602	-DLCAV-----YAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGP-----	650
Db	292	YELCGLLPATAYTLQIRCIWPLPGHWSWS-PS-----LELRTERAPTVELDTWWR---	343
QY	651	GDPMKKEKNVTLWPKMLKNDLSCSVQRYVINHTS-----CNGTWSDEGVNHTKF	701
Db	344	-QRLDPRTVOLFVKVPVLEEDSGRIQGYVWSNRPSQACAILPLCNTT-----ELSC	395
QY	702	TFLWTQAHYTVVLATNSIGASVANLNTFSWPMKVNIVQSLSAYPLNSCVIVSWLS	761
Db	396	TFHLPSAQEVALVAYNSACTSRPT-PVVES--ESRGPALTRLHAMARDPHSLWVGW--E	450
QY	762	PSDYKLMYFIIEW 774	
Db	451	PPNPWQGIYIEW 463	
RESULT 15			
S17308			
leukemia inhibitory factor receptor - human			
C:Species: Homo sapiens (man)			
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999			
C:Accession: S17308			
R:Gearring, D.P.; Thut, C.J.; VandenBos, T.; Gimpel, S.D.; Delaney, P.B.; King, J.; Price			
EMBO J. 10, 2839-2848, 1991			
A:Title: Leukemia inhibitory factor receptor is structurally related to the IL-6 signal			
A:Reference number: S17308; MUID:92007727			
A:Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-1097 <GEN>			
A:Cross-references: GB:X61615; NID:g34365; PIDN:CAAA43805.1; PID:g34366			

205	Db	WASDMPLECAIHFEVRCYIDNLFHPSGLEBWSOWSPVKNISWIPDSQTKVFPQDKVLWG	264
346	QY	SNVSFHCYYKKENKIIVSKEIVMMMLAEKIPQSYDVV---SDHVSKYTFNFNLNETKR	402
265	Db	SDITFCVV-----SQEKV---LSALIGHTNCPLIHLGDENVA-IKIRNISVASS	310
403	QY	GKFTYDAVYCCNEHECHRRYAEIYIVDVNINISCTDGHLYTKMCRWSTSTQSLA---E	459
311	Db	GT---NVVFTEDNIQGTIVFAGYPTDPOOLNCEPHD-LKEIKSWNPRVTALVGPRA	366
460	QY	STLQLRVHRSSLYCSDIPSIHPITSEPKDCVQLQSDGFECYIOPIFLLSGYTWKIRINHSL	519
367	Db	TSYTLVESFSGKYRLKRAEAPNES-----YQLFQMLPNQEIYNFTLNAHNPL	416
520	QY	GSLDSPPTCVLPDSVYVKPLPPSPVKAIEITINGLLKISWEKP-----VFPEN	566
417	Db	GRSQSTILVNITEKV-PTHPTSFVKV-DINSTAVKLSNHLPGNPAKINFLCEIEIKSN	474
567	QY	NLQFOIRYGLSGREVOKWVEYVDAKSVSLPVPDLCAYAVQVRCRDLGLGTWSNWS	626
475	Db	SVQEQRNVTIKGVE-----NSSYVALDKLNPYTLTYTRICS-TETFWKSWKS	523
627	QY	NPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNVTLLWKPLMKNSLCSQVRVYVNHHTS	686
524	Db	NKQHLTTEAS-PSKGPDTWRESSD-----GKNLIYWRPLPINEA-----NKGILSYNVS	574
687	QY	CNG-----TWSESDVGNHTKFTFLWTBQAHTVTVLAINSIGASVANFNTFSWPMKVNIV	741
575	Db	CSSDEETSLSLEIPDQHKRAEIRLDKNDYIIISVAKNSVGSPPSKIASMEIPNDDLKIE	634
742	QY	QSLSAVPLNSCIVSNIWILSPS---DYKLWYFIEWKV--LNEDGEIKWLRISS	791
635	Db	QYVGM-----GKGILLTAHWDPNMTCY-----VIKWCNSRSEPCPLMDWRKYKPSN	680

Search completed: October 22, 2001, 16:04:59
Job time: 69 sec

